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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    803.6
792.2
791
771
666.8
665.8
                                                                                                Score
                                                                                                Query
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Gapop 10.0 , Gapext 1.0
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BQ716569 AGENCOURT
BM921371 AGENCOURT
BM545444 AGENCOURT
BF339448 602039102
BG109391 602280448
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443	38 40 41	34 35 37	28 29 30 31	25 26 27	220	100 100 112 113 114 115
4- UI - U	370.4 366.6 359.2 358.2	381.2 377 375.4 374.2 371.2	442 415.4 405.4 387.8 384.2	479 477.8 479.4 459.4	537.8 510 507.4 495.8 486	39 39 39 39 39 39 39 39 39 39 39 39
7.88		30.0 29.7 29.6 29.5	00124	5677	42.4 40.2 40.0 39.1 38.3	44455 44455 44455
477 470 586 371	389 430 443	685 629 377 1015 1850	690 576 889 391 462	491 494 1006 762	745 531 794 815 487	796 644 717 933 627 882 912 883 835
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3718 5721 6951 0906	BE004365 AW744572 BQ723059 AA801465	AL543659 B1489863 N95751 BM544363 BC018871	BF104873 AW142226 BQ897144 BM699401 BE656312	BM707581 BQ695207 AL545549 B1834712	BG431026 BG431026 AW957458 B1837271 BG174360 AL041285 B1523975	BI453348 BG938621 BI251219 BQ716088 BF090699 BG716089 BF0930927 BI764020 BI764020 BQ718885
37185 zc51c05. 572176 xt75e10 695168 UI-E-CQ 090673 QV2-NT0	CMO-BNO1 ur32h12. AGENCOUR ST190962	1543 6030 65e0 AGEN	C C 70 H C	0555	6024 6024 6030 6023 6023	BI453348 603173067 BG938621 cn27c11 x BI251219 602994427 BQ715088 AGENCOURT BF090699 QV2-NT004 BI855121 603038662 BQ930927 AGENCOURT BI765916 603057118 BI766916 603043221 BQ718885 AGENCOURT BI183862 UNI-P-FM

## ALIGNMENTS

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FEATURES source		AUTHORS TITLE JOURNAL COMMENT	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BQ720516 LOCUS DEFINITION
http://image.llnl.gov plate: LLAM13583 row: f column: 05 High quality sequence stop: 634. Location/Qualifiers 1.996	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 996)	IMAGE:6188164 5', mRNA sequence. BQ720516 BQ720516.1 GI:21859413 EST. human.	BQ720516 996 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8219503 Lupski_sympathetic_trunk Homo sapiens cDNA clone

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BASE COUNT
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Matches 866
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                   CAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTAC
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Technologies."

284 C 242 g 224 t l others
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/clone="IMAGE:6188164"
/clone_1ib="Lupski_sympathetic_trunk"
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CCCGAGGCCTGCCGAGGAGACATGATGTGTGTTAACCAAAATGGCGGGTATTTATGCATT 132
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Query Match
Best Local Similarity
Matches 861; Conserv
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13581 row: c column: 21
High quality sequence stop: 646.
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National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT_8215248 Lupski_sympathetic_trunk
IMAGE:6187340 5', mRNA sequence.
BQ716569
BQ716569 GI:21855466
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 904)
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Location/Qualifiers
                                                                                                                                                                                  /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTACTTCTACACTCCCACGCGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo College of Medicine); available through Life Technologies."

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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:6187340"
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                                                                                Score 792.2; DB 14;
Pred. No. 2.2e-205;
D; Mismatches 18;
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AGENCOURT_6626255 NIH_MGC_115
5', mRNA sequence.
BM921371
NIH-MGC http://mgc.nci.nih.gov/.
national Institutes of Health, m
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
Email: cgapbs-r@mail.nih.gov
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1014)
                                                                              Homo sapiens
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                                                                                                          BM921371.1 GI:19371750
                                                                                                                                                                                            T---ACAAGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAG
                                                                                                                                                                                                                                            CATCAACGAATGTGAGCACAGGAACCACACGTGCAA-CCTGCAGCAGACGTGCTACAATT 847
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Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12787 row: i column: 10
High quality sequence stop: 738.
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                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Homo sapiens"
/db_xref."taxon:9606"
/clone-"IMAGE:5752785"
/clone_11b-"NIH_MGC_115"
/lab_host-"DH10B"
/note-"organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Similarity Conservative 62.3%; 98.2%; 0; Score 791; DB 14; Pred. No. 4.9e-205; Mismatches Length 1014; S Gaps

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Eukaryota, Metazoa, Chordata,
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 954)
1 (bases 1 to 700 nci.nih.gov
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12727 row: c column: 05
High quality sequence stop: 676.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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 TGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATGTGAACGAGTGT
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/db_xref="taxon:9606"
/clone="IMAGE:5729596"
/clone_11b="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                      /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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Mismatches 0;
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Mammalia; Butheria; Primates; Catar
1 (bases 1 to 891)
11 (bases 1 to 891)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mamm
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                                                                                                                  CAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAA-TGCATCGACCCCCATCCGCTGTGA 887
                                                                                                                                                                                                                                                                                                                                                                                                                  GACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTG 828
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GCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCG 1006
                                                                                                                                                                                                                            CAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAAGTGCATTGACCCCCATCCGCTGTGA
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/db_xref="taxon:96ub"
/clone="IMAGE:4186704"
/clone="IMAGE:4186704"
/clone="Ib=""NCI_CGAP_Brn64"
/tissue_type=""qlioblastoma with EGFR amplification"
/lab_host="DHIOB (T1 phage-resistant)"
/note=""Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Plate: LLAM10021 row: o column:
High quality sequence stop: 676.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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                                                                                                                                              TTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATC
AACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAA
                                         TTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATC
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hun
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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NIH-MGC http://mgc.nc1.nih.gov/.
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http://image.lln1.gov
Plate: LLAM11637 row: f column: 18
High quality sequence stop: 796.
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Mammalia;
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                                                                                                                                                                                      quality sequence stop:
Location/Qualifiers
  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal:
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d'
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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1 to 796)
                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5252369"
/clone_11b="NCI_CGAP_Mam5"
                                                                 /tissue_type="tumor, gross
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
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National Human Genome Research
10/10C101, 9000 Rockville Pike,
Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes
DNA Sequencing Center (NISC):
Intramural Sequencing Center (NISC):
Intramural Sequencing Center (NISC):
Intramural Sequencing Center (NISC):
Intramural Sequencing Communication (NISC):
Seq primer: -21M13 forward primer (ABI):
Seq primer: -21M13 forward primer (ABI):
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/tissue_type="Trabecular Bone Cells"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/lab_host="SURE"
/note="Organ: Hip; Vector: pBluescript; Site_1:
/note="Organ: Hip; Vector: pBluescript; Site_1: pBluescript; Site_1:
/note="Organ: Hip; Vector: pBluescript; Site_1: pBluescript; Si
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/db_xref="taxon:9606"
/clone="NHTBC_cn27c11"
/clone_lib="Normal Human Trabecular Bone
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution
Clone distribution the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image_llnl.gov
plate: LLAM11371 row: e column: 08
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Mutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

(bases 1 to 717)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                Similarity 89.8
36; Conservative
                                                                                                                                                  GCCCTCTTGTCTGCCCCCTTTGGGTATCAGATGAAGGCAACCAGTGTGTGGATGTGG
    GCGGGTACACCTGCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGTGCTTAGACA 430
                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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/strain="057BL/6J"
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/db_xref="taxon:150191"
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/tissue_type="tumor, gross tissue"
/tissue_type="tumor, gross tissue"
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/lab_host="DH10B"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo di
Site_2: Not1; Cloned unidirectionally. Investigators
Ilbrary constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
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pred. No. 5.9e-151;
0; Mismatches 72;
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musculus cDNA clone IMAGE:5150191 5',
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121 646 61 586 'n

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Contact: KODEL.

Email: GGapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CLONA Sequencing by: Agencourt Bioscience Corporation
CLONE distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM13588 row: e column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 ATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGC 958
                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 791
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1. (bases 1 to 933)
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AGENCOURT_8099803 Lupski_sympathetic_trunk
IMAGE:6190063 5', mRNA sequence.
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BQ716088.1 GI:21854985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTAC
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                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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QV2-NT0048-120900-360-all
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619; Conserv
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
1 kb for average insert length 1.9 kb. This is a primary
Ilbrary, non-amplified. Library constructed by Life
College of Medicine); available through Life
College of Medicine); available through Life
Technologies."
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284 c 245 g 179 t
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Pred. No. 2e-1
0; Mismatches
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 10 BQ716088 LOCUS

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DEFINITION

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AUTHORS TITLE JOURNAL EFERENCE

FEATURES

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Eukaryota;

Metazoa; Chordata;

Craniata;

Vertebrata;

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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson, \mathbf{A.J.} . Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
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                                                                                              GGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCAC 728
                                                                                                                                    CATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATAT
                                                                                                                                                        CATCTGCCGCTGTGACCCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATAT 668
                                                                                                                                                                                                            GAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTTT
                                                                                                                                                                                                                                                  GAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                          CATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCCTGGATCCTA 488
                                                          GGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCAC
148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D
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National Institutes of Health, M
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Clone distribution: MGC clone distribution information can
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                                                                                                                                         /note-*organ: pooled brain, lung, testis; Vector: pcMV-SpORT6; Site_1: Noti; Site_2: EcoRV (destroyed); RN7 source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 18 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Carnber (Invitrogen). Research Genetics tracking code
                                                                                              Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library." 277 c 216 g 197 t lothers
                                                                                                                                                                                                                                                                                                                /clone_lib="NIH_MGC_115"
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EST.
house mouse.
                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arayed by: The I.M.A.G.E. Consortium
CLONE Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM13960 row: d column: 05
High quality sequence stop: 651.
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National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTGTGCATCCCTCGAACCAACCCAGTGTATCGAGGGCCCTTACTCAAATCCCTACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTCG
                                                                                                       GCAGTGATATGGACGAGTGCAGCCTTCTCCCGAGNTTCCTCTGTCAACACGAGTGTGTGGA
                                                                                                                        GCAGTGATATGGACGAGTGCAGC--TTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAA
                                                                                                                                                                                                          CAAGATGTGAACGAGTGCGAAACTGAGAATCCCTGTGTTCAGACCTGTGTCAACACCTAT
                                                                                                                                                                                                                                                           GGATCCTATTCCTGTACATGCAACCCTGGTTTCACCCTCAACGACGATGGAAGGTCTTGC
                                                     ACAGCCGGGCTCATACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa. site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 248 c 208 g 212 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N-3"
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/lab_host="DH10B"
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                                                                               734
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722 600 540 602 480 542 420 482 360 422 300 362 240 302 180

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JOURNAL COMMENT
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AUTHORS
TITLE
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI768516 912
603057118F1 NIH_MGC_122 Homo
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Tissue Procurement: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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CCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACA 1063
                                                                                                           GCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCT 1003
                                                                                                                                                                                                  GTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTG 943
                                                                                                                                                                                                                                                                                       ACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCT 883
                                                                                                                                                                                                                                                                                                                                                                            TGGATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCA 823
                                                                                                                                                                                                                                                                                                                                                       TGGATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCA
                                                                                                                                                                           GTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTG
                                                                                                                                                                                                                                                                ACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTCAAATGCATCGACCCCATCCGCT 180
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="pHIOB"
/lab_host="pHIOB"
/note="Corgan: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Corgan: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Corgan: pooled lung and spleen; RNA source
site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

30 a 262 c 225 g 195 t
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/db_xref="taxon:9606"
/clone="IMAGE:5206588"
/clone_lib="NIH_MGC_122"
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 564.4; DB 13; Pred. No. 3.8e-143;
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RESULT 15
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Best Local S
Matches 619
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JOURNAL
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                                                                               619;
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: i column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae.

1 (bases 1 to 880)
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BI764020
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603043221F1 NIH_MGC_116 Homo
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                                                                                                  Similarity
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                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 846.
                                                                             Conservative
                                                                                                                                                                          /note-*Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORY (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcORV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5183693"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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                                                                                              43.3%;
                                                                             0;
                                                                             Score 549.6; DB 13;
Pred. No. 4.1e-139;
0; Mismatches 4;
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sapiens cDNA clone IMAGE:5183693 5',
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                                          CCTACGGCTCTTTCATCTGCCGCTGTGACC 625
             TTGCCAAGA-TGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCCTGCGTCAACA 595
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Search completed: July 3, 2003, 17:36:08 Job time : 1873.78 secs

	1562 1843	3 GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGA 	1503 1784
	1502 1783	CAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGTCGCA	1443 1724
	1442 1723	GATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGT	1383 1664
	1382 1663	TGGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGT	1323
	1322 1603	CTTCCAAATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATC	1263 1544
	1262 15 <b>4</b> 3	CTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACAT	1203 1484
	1202 1483	GAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCC	1143 1424
	1142 1423	CTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCT	1083 1364
	1082 1363	CTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTG	1023
	1022 1303	GCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAG 	963 1244
	962 1243	CAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAAACCA	903 1184
•	902 1183	CGGCTCTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG	843 1124
	842 1123	CCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCAACACCTA	783 1064
	782 1063	TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG 	723 1004
	722 1003	GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC 	663 944
	662 943	CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA	603 884
	602 883	TGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCAGCCCAGATCTGCAT 	543 824
	542 823	CACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATG	483 764

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Prior Application removed - St
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
US-10-180-557-407
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Gestoyers, Luc
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: When I Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watan
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US-10-180-557-407
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CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrap
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APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddwski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Hood, William I.

APPLICANT: Lhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C153

CURRENT APPLICATION NUMBER: US/10/180,552

CURRENT EILING DATE: 2002-06-25

PTIOT ADDITATION OF THE SAME

FILE REFERENCE: P3430R1C153
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NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 407
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-552-407
                                                                                                                                                                                                                                                         Sequence 407, Application US/10180552 Publication No. US20030022300A1 GENERAL INFORMATION:
                         Query Match
Best Local Similarity
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                       Score 2322.8;
Pred. No. 0;
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Poll J.
APPLICANT: Goddward, Poll J.
APPLICANT: Goddward, Poll J.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: When J. Secreted and Transmembrane Polypeptides and Title Of Invention: Secreted and Transmembrane Polypeptides and Title Of Invention: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/176,913
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
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RESULT 13 US-10-176-913-407 ; Sequence 407, Application US/10176913 ; Publication No. US20030022298A1 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P.		Db 2384 GGTTTÄATTCTGTCTTGTTCÄTTTTGÄGTATTTTÄÄÄÄÄÄÄÄTÄTGTCGTÄGÄÄÄÄTTCCTTC 2443  Qy 2163 GAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCCATTTT 2222	Db 2264 GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAA 2323  Qy 2043 AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAAC 2102  Db 2324 AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCCAGTTGTCCTTAAATTTGTATAAC 2383  Db 2324 AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTTCAGTTGTCCTTAGAATTTCGTAGAATTCCTTC 2162  Qy 2103 GGTTTAATTCTGTTCTTCTTCTTTGAGTATTTTTTAAAAAAATATGTCGTAGAATTCCTTC 2162	Qy         1923 CAAAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTTGCTT		1964 CCTGTCAC 1743 ATCATTGC         2024 ATCATTGC	1623 CTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGA	1784 GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTCCCCATTGGCACCCAAGGGA  1563 CAGGAGAAGAGAGAATAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTCCTG	Qy 1443 CAACACTGTCAACTTCAGAGGCAGCTCCGTGATCCGGACTGCGGATATATGTGTCGCA 1502	Db 1604 TGGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGT 1663  Qy 1383 GATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTTGGAAATGATCACTGT 1442

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APPLICANT: Zhang, Zemin

ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLITIFIE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430RLC86

CURRENT APPLICATION NUMBER: US/10/176,757

CURRENT EILING DATE: 2002-06-20
PILOT Application removed - See File Wrapper or F
NUMBER OF SEQ ID NOS: 612

SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien

US-10-176-757-407

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Sequence 407, Application US/10176757
Publication No. US20030022297A1
GENERAL INFORMATION:
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Gurney, Austin 1
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Best Local Similarity
Matches 2324; Conserv
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GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Chen, Jian

APPLICANT: Chen, Jian

APPLICANT: Godowski, Paul J.

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

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TITLE OF INVENTION: SECRETED AND THE SAME

FILE REFERENCE: P3430R1C70

CURRENT APPLICATION NUMBER: US/10/176, 482

CURRENT FILING DATE: 2002-06-20
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	AAATGCATCG	7	CTGGATCGCC	TECCE ACCAC	TGCCGAGGAG 	AACCCTGTGT	AACCCTGTGT	CCAGCAGCTG	CCAGCAGCTG	reccectite	receering	ACAGATTCCC	GAGTBYGCAACAGATTCCCACCAGTG	GGGTACACCTGCTCCTGCACC	CGCTATGGTT	CGCTATGGTT	AACCCTGGTT	AACCCTGGTT	ACCGAGAACCC 		GACCCAGGAT 	TTCTCTGAGT		11010101010	TGCCCTCCAG	TECCCTCCAC	GAGCACAGGA		GAGCACAGGA	AAATGCATCG	AAATGCATCG	
	ACCCCATCC	GTCTTCCAAG	AGTCAGGAC <i>P</i>	AGTCAGGACA	ACATGATGTG	ATCGAGGGCC		CCCCACCACT	AGCAGCTGCCCCACCACTCTC	GATACCAGA	GATACCAGAS	ACCAGTGCA	ACCAGTGCATA	CCGACGGATA	ACTGCCAGC	ACTGCCAGCA	TGGTTTTACCCTCAL	Ci	CIGCO FILL SODED		ATGAACTTG	TCCTCTGCC		100101000	GCTACATCC	GCTACATCC	ACCACACGTO		ACCACACGT	HILLILL	ACCCCATCC	
	CTGTGAGGA	#CTCACTCTTACCATTCTGCCTCTCTGTCTTCTAGCCCCTGGGAAF: 	NTGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTAGATATT	GTGTTTAGAT	GAGGAGACATGATGTGTGTTAACCAAAATGGCGG 	CCTACTCGAACCC	≥=	CTCAGCTCC	CTCAGCTCCAAACTATC	CTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGC	AGATGGATGAAAGCAAC	CAACCCCACCCA	TTCCCTTTCTCAAC	TGCACCGACGGATATTGGCTTCTGGAAG	AGCTCTGTGC	GCTCTGTGCGAATGT		CAATGAGGATGG	TGCAAACCTGCGTCAAC		TTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG 	ACATGAGTG		STORE SHOTE	CTACATCCTGCTGGATGACAACCGAAG	GCTGGATGA	TGC	를 등 등	CAACCTGCA	CCATCCGCTGTGAGGAGCCTTATC	CTGTGAGGA	
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CAGTGTTTTCT	SGCCTTCAGA	AAATGCAAG	ATGAGGGCA(           ATGAGGGCA(	CACGCCCCA	CACGCCCA	CTGTCATCA	CTGTCATCA		CARTITIONS		CCTTTCCCC	CGTTTCCCC	CACCCTGCA	CACCCTGCA	TGCTCCCCT	TOCICCOL.	TTCAAAGAA	CTTGCTGTC	CTTGCTGTC	ACCCGGGAG	BACCCGGGAG	AGGCTATGTA	AGGCTATGTA	ATGCCTGGTA	TGCCTGGTA		AATTCTGTC	PAATTCTGTC	GCCTTCAGA	GCCTTCAGA		TGTTTT
TTGAGGAC	CACATGCTAT	CTTCCAAATGCAAGCCACGACCCGCTACCACGATTTTCCAGATCAAATC	TGGGAATGAGGCCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCCACCCTGGT	GATGACACGCCCCATCAAAGGGCCCCGGGAAATCCCAGCTGGACTTGGAAATGATCACTGT	CAAAGGGCC	CAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCA	ACTICAGAGG	GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTCTCATTGGCACCAAGGA	CICGGGCIG		SAAGAGTCAG	CTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGA	CCTGTCACCCTGCAGGACTTGCCACCCCCCAGTTCCTATGATACAGTTATCAAAAAGTATT	GACTTGCCA	ATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTTCAAGGCCTTCAGTTATTTTTTTT	PATAGATTAG		ACTTCTTCAC	AACAGCTIGCTGTCACTTCTTCACCTCTTCCACTCTCTCACTGTTACTGCTTTG	CTGGCGGGGA	CAAAGACCCGGGAGCTGGCGGGAACCCTGGGAGTAGCTTTGCTTTTTGCGTACACA	GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAA	AACAAACCAC	TTTCAACCA	ACCATGCCTGGTATTTTCAACCATAAAAGTATTCAGTTGTCCTTAAATTTGTATAAC		GGTTTAATTCTGTCTTGTTCATTTTGAGTATTTTAAAAAAAA	TTGTTCATTT	CACATGCTAT			TTGAGGAC
CCCTTAATCTT	GITCIGICI	CTACCCTGGG	CATGCGGCAP                         CATGCGGCAP	CCGGGAAATC	CCGGGAAATC	CAGCTCCGTG	CAGCTCCGTC		CACAATCACA		CCCGACTTO	CCCGACTTC	CCCCAGTTO	CCCCAGTTC	TGTTGGTGA	TOTAL COLUMN	GITTGCGGG	CTCTTCCACT	CICTICCACT	ACCCTGGGA	ACCCTGGGA	AGCAGGATCO	AGCAGGATCO	TAAAAGAAGT	TAAAAGAAGT	TCACTATORY	TGAGTATTT	TGAGTATTT	GTTCTGTCTT	GTTCTGTCTT		CCTTAATCT
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RESULT 9
US-10-175-738-407
Sequence 407, Application US/10175738
PUBLICATION NO. US20030022294A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Thang, Zemin
APPLICANT: Thang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430R1C45
CURRENT FILING DATE: 2002-06-19
PRIOT APPLICATION NUMBER: US/10/175,738
CURRENT APPLICATION TEMOVED - See File Wrapper or Pa
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
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Matches 2324; Conserv
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                                           Score 2322.8;
Pred. No. 0;
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RESULT 8
US-10-173-706-407
; Sequence 407, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: EARNY, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION UNDEER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
PRIOT APPLICATION UNDEER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
PRIOT APPLICATION TO SECOND NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
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US-10-175-737-407
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES (
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343871C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
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APPLICANT: Baker, Kevin
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Gurney, Austin L.
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo is Organism: 15-10-176-758-407
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Sequence 407, Application US/10176758

Publication No. US20030008353A1

GENERAL INFORMATION:

APPLICANI BAKET, Kevin P.

APPLICANI Chen, Jian

APPLICANI Chen, Jian

APPLICANI Godowski, Paul J.

APPLICANI Godowski, Paul J.

APPLICANI Godowski, Paul J.

APPLICANI Godowski, Paul J.

APPLICANI Smith, Victoria

APPLICANI Watanabe, Colin K.

APPLICANI Watanabe, Colin K.

APPLICANI Watanabe, Colin K.

APPLICANI Watanabe, Colin K.

APPLICANI Watanabe, Zemin

ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POI

TITLE REFERENCE: P3430RAC104

CURRENT APPLICATION NUMBER: US/10/176,758

CURRENT FILING DATE: 2002-06-21
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or NUMBER OF SEQ ID NO 407
LENGTH: 2609
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Best Local Similarity
Matches 2324; Conserv
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10	APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-1 FILING DATE: 1998-1 APPLICATION NUMBER: FILING DATE: 1999-0 APPLICATION NUMBER: FILING DATE: PROPER: FILING DATE: P	R FILING DATE: 1999-08- R APPLICATION NUMBER: 0 R APPLICATION NUMBER: 0 R APPLICATION NUMBER: 0 R APPLICATION NUMBER: 0 R FILING DATE: 1999-08- R FILING DATE: 1999-10- R FILING DATE: 1999-10- R APPLICATION NUMBER: 0 R FILING DATE: 1999-11- R APPLICATION NUMBER: 0 R FILING DATE: 1999-11- R APPLICATION NUMBER: 0 R FILING DATE: 2000-03- R FILING DATE: 2000-04- R APPLICATION NUMBER: 0 R FILING DATE: 2000-09- R APPLICATION NUMBER: 0
Db 1184 CAGTGATATGGACGAGCTGCTAGAGTTCCTCTGAGTTCCTCTGAGCAAGATGAGTGTGAACCA 1243  Qy 963 GCCGGCACATACTTCTGCTGCTGCCCTCCAGGCTACATCCTGCTGGATGACCAAG 1022	Db 944 GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAAGGTCTTG  Qy 723 TGGATCCTATTCTTGATGAATGTCGCTATGGTTACCCTCAATGAGGATGGTAGGTCTTG  Qy 723 TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG  Db 1004 TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG  Qy 783 CCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCAATGAGGATGGAAGGTCTTG  Qy 1	Oy  63 GCGAGCCCCGAGGGCCCAGAGGAGGCCGACTGCCCGAGCTCCCCGCCCCG

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3130R1C7
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OR APPLICATION NUMBER: 60/059588
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062816
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063329
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                                                                 FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/066840
FILING DATE: 1997-11-25
APPLICATION NUMBER: 60/069694
FILING DATE: 1997-12-16
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APPLICATION NUMBER: 60/066364
APPLICATION 1997-11-21
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P.Mickey Williams
William I. Wood
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Margaret Ann Roy
Timothy A. Stewart
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David A. Botstein
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FILING DATE: 1998-08-19
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APPLICATION NUMBER: 09/114844
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APPLICATION NUMBER: 60/145698
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2223 AGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTTCTTT	l oy	•
2376 GAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTTCCATTTT 2435		Db
2163 GAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCCTCTCCCATTTT 2222	3 CTACAATTTACAAGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCT 114	δ
2103 GSTTTAATTCTGTCTTGTTCATTTTUGAGTATTTTTAAAAATTATGTCGTAGAATTCCTTC 2162 	1023 CTGCCAAGACATCAACGAATGTGAGCACAGAGGAACCACAGGTGCAACCTGCAGGAGACGTG 1082	Db Qy
	963 GCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACCAGCCGAAG 1022	Ор
	903 CAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCCTCTGCCAACATGAGTGTGTGAACCA 962	Оy
	843 CGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG 902	Qy Db
AACAGCTTGCTGTCACTTCTTCACCTCTTCCACTCCTTCTCACTGTGTTACTGCTTTG	783 CCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCCTGCGTCAACACCTA 842	. Qy
CTATTTTCAAKGAAATAGATTAGGTGGGGGTCTGAGTCTATGTTCAAKGATGTG 	723 TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG 782	Qy Db
ATCATTGCTCCCCTGATAGAAGATTGTTGGTCAATTTTCAAGGCCTTCAGTTTATTTCCA 180	663 GTGCTTAGACATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC 722	Фр
CCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGCATACAATATGCAAAAAGTATT   +	603 CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA 662	Qy Db
CTGAAGGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTGTCACCTGTACTATTGCAGA	543 TGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCAGCCAG	Qу
CAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACAGAGGTTAGGCATTFCCTG 162	483 CACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGAAGCAACCAATG 542	Оу
503 GTACCCATTCTCAGCCTCGGGCTGGAGCCTCCGACGCTCCTCATTGGCACCACGGA	423 GACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGGCTCCAAACTATCC 482	Qy
CAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTCTCGCA	363 GTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTC 422	Qy db
GATGACACGCCCGATCAAAGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGT 	303 ATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTAACCAAAATGGCGG 362	Qy Db
	ATTGATGA 302          ATTGATGA 515	Qy Db
CTTCCAAATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATC [	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Qy Db
1203 CTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACAT 1262	123 CGAGCTTTCTTCGCCTTCGCATCTCCTCCTCGCGCGTCTTGGACATGCCAGGAATAAA 182	Qy Db
1143 GAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCC 1202 	63 GCGAGCCCCGAGGGCCCAGAGGACGACGTGCCCGAGCTCCTCCGGGGGGTCCCGCCCG	Qу Db

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                                                                              GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTTCAA
                                                                                                                                             CAAAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTTGCGTTACACA 1982
                                                                                                                                                                                            ACAGCTTGCTGTCACTTCTTCACCTCTTCCACTCCTCTCACTGTGTTACTGCTTTG
                                                                                                                                                                                                                                                                                                                                           ATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCA 1802
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                                                                                                                            CAPAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCCTTTTTGCGTACACA
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Patent No. US20020038006A1
GENERAL INFORMATION:
                                                       Matches 2325;
                                                                    Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/212,168
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-03:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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Corley, Neil C.
Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX
NUMBER OF SEQUENCES: 6
                                                                                                                                                                  TOPOLOGY: 11
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
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FILING DATE: 16-Apr-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
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                                                                    Similarity
COUNTRY: US
ZIP: 94304
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STATE: CA
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Pred. No. 0;
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Sequence 1, Application US/09083002
Patent No. US20010016650A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Racle, Lisa A.
APPLICANT: LaValile, Edward R.
APPLICANT: LaValile, Edward R.
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Chery1
APPLICANT: Evans, Chery1
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Tashiro, Kei
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                                         ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
                                                                                                                                                        APPLICANT: Nakamura, Tomoyuki
TITLE OF INVENTION: SECRETED PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
APPLICATION NUMBER: US/09/083,002
       STRANDEDNESS: doi
TOPOLOGY: linear
DLECULE TYPE: cDN
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CLASSIFICATION:
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Best Local Similarity
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ IL
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    Published_Applications_NA: *
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US-10-176-752-407
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## ALIGNMENTS

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/041,016
FILING DATE: 07-Jan-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                  APPLICATION NUMBER: US/09/083,002
FILING DATE: 21-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED PROTEINS NUMBER OF SEQUENCES: 2
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TELEFAX: (617) 876-5851
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Evans, Cheryl
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LOCATION:
PCT-US95-02251-2
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NAME: Parker David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UMIC009P--

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924

INFORMATION FOR SED ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3753 base pairs

TYPE: nucleic acid

STANDENNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FRATURE:

FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%;
Best Local Similarity 49.1%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            2452 GGTGACTGCATCAATACCAATGGTTCCTACAGATGTCTCTGTCCCCTGGGTCATCGGTTG 2511
2512 GTGGGCGGCAGGAAGTGCAAGAAAGATATAGATGAGTG 2549
                                        1006 CTGGATGACAACCGAAGCTGCCAAGACATCAACGAATG 1043
                                                                                                                                                                           2392 AGGGATCGGAGCCGCTGTGAGGACATTGATGAATGTGACTTCCCTGCGGCCTGCATCGGG 2451
                                                                                                                                                                                                                                                                   2332 ATCTGCACGAACACACCAGGCTCTTTCCAGTGTCAGTGCCTCTCCGGCTATCATCTGTCA 2391
                                                                                                                                                                                                                                                                                                                                                          2272 GGACGCCTCAGTTGCATAGACGTGGATGACTGTGAGGCTGGGAAAGTGTGCCAAGATGGC 2331
                                                                                                                                                                                                   886 GAAGATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAA 945
                                                                                                                                                                                                                                                                                               826 ACCTGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAG 885
                                                                                                                               946 CATGAGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTG 1005
                                                                                                                                                                                                                                                                                                                                                                                      769 GATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACGAGAACCCCTGC---GTGCAA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.6; DB 5; Length 3753; Pred. No. 7e-05;
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Search completed: July 3, 2003, 17:40:01 Job time : 109.424 secs

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RESULT 14
PCT-US95-02251-17
; Sequence 17, Applicat.
; GENERAL INFORMATION:
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMICO09P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPEAX: (713) 789-2679
TELEX: 79-0924
                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5502 base pair
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US O
FILING DATE: 30-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 18-FEE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                  nucleic acid
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 linear
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18-FEB-1994
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                 single
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CELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ME
TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                              PRIOR APPLICATION DATA:
                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                 STATE:
                        APPLICATION NUMBER: FILING DATE: 30-SE
                                                                               CLASSIFICATION
                                                                                                  FILING DATE:
                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                    CITY: Houston
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
           CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724 GGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCCTCAATGAGGATGGAAGGTCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCT 1137
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                                                                                                                                                                                                                                                                                               Texas
                                                                                                                                                                                                                                                                                                                                  E: Arnold,
P.O. Box 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                 PatentIn Release #1.0,
#1.30
                                                                                                                                                                                                                                                                              United States
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/desc = "DNA"
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                                                                                                  CONCURRENTLY
                          30-SEP-1994
                                                                                                                                                                                                                                                                                                                                       d, White: 4433
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CELLS
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                                         US 08/316,650
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RENTLY HEREWITH
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                                                                                                                                                                                                                                                                                  America
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                                                                                                                                                                                                                                                                                                                                                        Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                FOR STIMULATING
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                                                                                                                                                                                                                                                                                                                           Matches 167;
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    08-479-722B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: 30-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                 2395 AGGGATCGGAGCCGCTGTGAGGACATTGATGAATGTGACTTCCCTGCGGCCTGCATCGGG 2454
                                                                                                                                                                                                                                                   2215 TGTGAGAACCTTCCGGGTTCTTACCGTTGCACGTGTGCCCAGGGGATACGAACCCGCACA 2274
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                                                                  886 GAAGATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAA 945
                                                                                                                                         826 ACCTGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCCAGGATATGAACTTGAG 885
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946 CATGAGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTG 1005
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76 Hillmont, Suite 250
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AND METHODS
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Best Local Sin
Matches 223;
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Yin, Wush
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                  NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,48
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 934-7000
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DESCRIPTION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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STATE:
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                                               3121 GGCTCCTTTAGATGCTCCTGTGAGCCGGGCTATGAGGTCACCCCAGACAAGAAGGGCTGC
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724 GGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGC 783
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                        Score 52.4; DB 3;
Pred. No. 5e-05;
0; Mismatches 241;
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APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210.21.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 340
LENGTH: 220
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                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(220)
OTHER INFORMATION: n = A,T,C or
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                                                                               601 ATCAATACTGAAGGCGGGTACACCTGCTGCTGCACCGACGATATTGGCTTCTGGAAGGC
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              CAGTGCTTAGACATTGATGATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTT 720
GAGTGTGTGGACATAGACGAGTGCCGCTACCGCTACTGCACCGCTGCACCGCTGCACCGTTGAACCTG
                                                           CATAACTTGCCTGGCTCCTATCAGTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCC
                                                                                                                         TGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCCGGGAAATCCAGCTGGACTTGGA 1430
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                                                                                                                                                                                          Conservative
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    Mismatches

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Pred. No. 5.7e-14;
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Pred. No. 1.6e-16;
0; Mismatches 168;
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                                                                                                                                                                                                                   Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 164;
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INFORMATION FOR SEQ ID NO:
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MEDJIM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 2461 base pair
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CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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Similarity 54.5%;
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                                                                                                                                                                                                                                CGGAGGCCTGCGGGAGGCGCGCTGCAAGAACCTGCCCGGCTCCTACTCCTGCCTCTGTG
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                                                                                                                                                                                                                                                                                                                                                      ACGGGGGCTGCCTCCAGATCTGCCACAACAAGCCGGGTAGCTTCCACTGTTCCTGCCACA
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                                                                                                         -TCTGCAGGGCCGCTGTGAGCAGGTCTGCGTGAACTCCCCAGGGAGCTACACCTGCCACT
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Manfioletti, Guidalberto
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Avanzi, Giancarlo
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Pred. No. 6.4e-07;
0; Mismatches 128;
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US-08-897-443-2
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3373 base pair
TYPE: nucleic acid
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-5555
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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STATE: CA
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               3373 base pairs
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Corley, Neil C.
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US-09-643-597-278
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Best Local Sim
Matches 211;
                                                                                                                                                                   SOFTWARE: F
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                                                                                                                                                                                                                                                            APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
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                                                                                            TYPE: DNA ORGANISM: Homo sapien FEATURE:
                                 NAME/KEY: misc_feature LOCATION: (1)...(401) OTHER INFORMATION: n =
                                                                                                                                                   ENGTH: 401
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LIBRARY: UTRSNOT02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980 ACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTTGTGGACTACTGTGCCTCAGAAAAACC
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Similarity 57.7%;
                                                                                                                                                                                         FastSEQ for Windows Version
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Bangur, Chaitanya (
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Pred. No. 3.9e-21;
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GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
INUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 259
LENGTH: 1018
TYPE: DNA
ORGANISM: Human
US-09-188-930-259
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Patent No.
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                ACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGC 1405
                                                                                     GCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTT 1345
                                                                                                                  TCTGCCCGGCCTCCAACCCTCTATGTCGAGAGCAGCCTTCATCCATTGTGCACCGCTACA
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TCTACCCCGGTGCCTACAATGCCTTTCAGATCCGTGCTGGAAACTCGCAGGGGGACTTTT
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Pred. No. 1.9e-87;
0; Mismatches 321;
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; ORGANISM: HOMO
US-09-248-757-1
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US-09-248-757-1
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SOFTWARE: PatentIn Ve
SEQ ID NO 1
LENGTH: 2512
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Best Local
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CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STONE, EDWIN M.
APPLICANT: SHEFFIELD, VAL C.
APPLICANT: INVENTION: MACQULAR DEGENERATION DIAGNOSTICS
FILE REFERENCE: UIA-018.02
1051 AGGAACCACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTCAAATGC 1110
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                                                            CCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCAC
                                                                                                              GAGTTCCTCTGCCAACATGAGTGTGTGTAACCAGCCCGGCACATACTTCTGCTCCTGCCCT
                                                                                                                                                                                       GGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCT 930
                                                                                                                                                                                                                                                                                      CCATATTGCCACCAAAGATGCGTGAATACACCAGGCTCATTTTATTGCCAGTGCAGTCCT
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                               CAGGGATA - - - CCAAGTGGTGAGAAGTAGAACATGTCAAGATATAAATGAGTGTGAGACC
                                                                                           GGATATGAGCTAAGCAGTGACAGGCTCAACTGTGAAGACATTGATGAATGCAGAACCTCA
                                                                                                                                                                                                                        AACCCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCA 870
                                                                                                                                                                                                                                                                                                                    GGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAG
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Pred. No. 9e-61;
0; Mismatches 446;
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                                                         Best Loc
Matches
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                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/9
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
TITLE OF INVENTION: EIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                  MMEDIAL
LIBRARY: BRSING
TONE: 2786449
                                                                        Local
                                                                                                                                                                                                     TOPOLOGY: 11
                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
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                                                     Score 386; DB 3; Length 20
Pred. No. 2.5e-103;
0; Mismatches 400; Indels
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                                                                          GGGAGCCACCCTCCCTGCAGCT 1568
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US-08-833-963C-1
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08833963C Patent No. 5916769
GENERAL INFORMATION:
APPLICANT: Olsen, et al.
TITLE OF INVENTION: Extracellula:
TITLE OF INVENTION: HCABA58X
                        SOFTMARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,963C
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/05033
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 208
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CITY: Rockville
STATE: MD
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                                                                                                                                                                    Release #1.0, Version #1.30
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US-08-833-963C-1
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 1531 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
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39; Conservative
CGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTT 1344
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENCTH: 1260
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Best Local Similarity 85.1
Matches 1064; Conservative
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Pred. No. 2.3e-253;
5; Mismatches 150;
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Query Match  99.8%; Score 2324.4; DB 4; Length 2550; Best Local Similarity 100.0%; Pred. No. 0; Matches 2325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  Qy 3 CCCGGCGCTCTCCCGCTGTCCTCTCCACGACTCGCTCTGGAATAAAACACCC 62	INFOR SEQ SEQ I T T IMM IMM C C C C C C C C	APPLICATION NUMBER: US/09/212,168 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/884,072 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: B111ngs, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0333 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555	APPLICANT: Gueglér, Kar TITLE OF INVENTION: HUM NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: Incyte pha STREET: 3174 PORTER D CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE COMPUTER: IBM COMPATING SOFTWARE: FASTESE DOS SOFTWARE: FASTESE OF FORM:	- ຄື ຕິວສ	Qy 2163 GAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCCATTTT 2222
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1023 CTGCCAAGACATCAACGAATGTGAACCACAGGAACCACAGGTGCAACCTGCAGCAGACGTG 1082		GTGCTTAGACATTGATGAATGTTCGCTATGCTTACTGCCAGCAGCTCTGTGCGAATGTTCC	423 GACCCCCTACTCAGGTCCCAGCAGCAGCAGCACCACCACTCTCAGCTCCAAACTATCC 482		123 CGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCGTCTTGGACATGCCAGGAATAAA 182

99	P B	Qy	Db Qy	D	Qy	dy Qy		Db .	Q E	P 09	ОУ	Дy	B 5	 P	ρy	Db V	DB Qy	ОУ	Db Qy	Db .	φ <u>ξ</u>	2 29	Match
1023 CTGCCAAGACATCAACGAATGTGAGCACAGGAACCACAGGTGCAGCTGCAGCAGGTGCTGCAGCAGGTGCTGCAGCAGGTGCTGCAGCAGGTGCAACGTGCAGCAGGTGCAACGTGCAGCAGACGTGCAGCAGAGGTGCAACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGACGTGCAGACGTGCAGCAGACGTGCAGCAGACGTGCAGCAGACGTGCAGACAGGTGCAACACGTGCAGCAGCAGACACACAC	176 CCCCGGCATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAA 123	102	903 CAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCA 962 	1056 CGGCTCTTTCATCTGCCGCTGTGACCCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG 1115	43 CGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG 902	783 CCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCCTGCGTCAACACCTA 842 	723 TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG 782		3 GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTTCC 7	9 66	543 TGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCAGCCAG	483 CACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATG	#23 GAUCECCIACTEAGGICCGTACCCAGCIGCCCCACCACTETCAGCICCAAACTAICC 482	76 GTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTC 63	363 GTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTC 422	303 ATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTAACCAAAATGGCGG 362 	243 ACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTAGATATTGATGA 302	183 AAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAAGCCCTGGGAATGCACAGGC 242 	123 CGAGCTTTCTCGCCTTCGCATCTCCTCCTCGCGCGCTCTTGGACATGCCAGGAATAAA 182 		216 CCCGGCGCTCTCCCCCGTGTCCTCTCCACGACTCGCTCGGGCCCCTCTGGAATAAAAAACACCC 275 63 GCGAGCCCCGAGGGCCCAGAGGAGGCCGAACGTGCCCGAGCTCCTCCGGGGGGTCCCGCCCG	3 CCCGGCGCTCTCCCCGTGTCCTCTCCACGACTCGCTCGGCCCCTCTGGAATAAAACACCC 62	es 2325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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2316 GGTTTAATTCTGTCTTGTTCATTTTGAGTATTTTTAAAAAATATGTCGTAGAATTCCTTC 2375	2200 AACCATECCTESTATTTTCAACCATAAAAAAAAATTTTTAAAAAAATATGTCGTAGAATTCCTTC 2162	AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTTGTATAAC		2130 CAAANANUUUUGGGAANUUUTIGGAANATARGIITIGUITITTITTITTITTITTITTITTITTITTITTITTITTI	CAAAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCCTTTTTGCGTACACA	1863 ARCAGOTTGOTGTGACTTCTTCACCTCTTCCACTCCTCTCCACTGGTTACTGCTTTG 1922		1956 ATCATTGCTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTT	1743 ATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTTCAAGGCCTTCAGTTTATTTCCA 1802	1896 CCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGATACAGTTATCAAAAAGTATT 1/42 1896 CCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTATCAAAAAGTATT 1955	CTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGA	CTGANAGGETTETTGCCGANGAGTATACCAGGENGCAGAGGCGACCAGGACGTTAGGCAGGACGAGAGGCATTTCCTG	1716 GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGA 1775	GTACCCATTCTGAGCCTCGGGCTGGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGA	1443 CAACAOTGTCARCARACTTCAGAGGCAGCTCCGTGATCCGACTGCGGARTARTGTGTCGCA 1502 	GATGALANGCCCCATCARANGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGACCACTGT 	TOGGAATGAGGGCATAAAAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGT		TITLE A SATION DE CONTROL DE CONT	1356 GAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAGACCCTGGCTGCAGAGACCCAGCC 1415	1143 GAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCCTGGCTGCAGAGACCCAGCC 1202	1000 CIRCHALLICANOSUSUSCILICANTISCA CONTOCCCCATOCOCISIONOSMUCLIAICE 1146 1101	

GenCore version Copyright (c) 1993 - 2003

5.1.6 Compugen Ltd.

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Result
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             Sequence 17, Appl
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## ALIGNMENTS

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US-08-884-072-2
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Query Match
Best Local Similarity
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTENE DOS
SOFTWARE: FASTENE FOR WINDOWS Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,072
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: CORNN
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CITY: Palo Alto
STATE: CA
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ZIP: 94304
                                                                                                                                         TYPE: nucleic STRANDEDNESS:
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Search completed: July 3, 2003, 11:59:30 Job time : 522.747 secs

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A55 protein; mouse; smooth muscle proliferation; tissue generation; wascular smooth muscle cell; arteriosclerosis; tissue reparation; my vascular endothelial thickening; haematopoietic cell-regulator; cytipercutaneous transluminal coronary angioplasty; blood coagulation; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy; tumour metastasis inhibitor; ss.
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This sequence encodes the mouse A55 protein. The invention relates to th human A55 protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, and a catherin/tumour metastasis inhibiting activity; tumour inhibition, and a catherin/tumour metastasis inhibiting activity; tumour inhibition, and a
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Sequence 2429
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Matches 1795; Query Match Best Local Similarity Conservative 62.3%; 0; Score 1449.8; Pred. No. 0; Mismatches 333; DB 21; Indels Length 26; Gaps

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Matches 1795;
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        AACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCAG
                                                                                                      GGGAATGAGGGCAGAGAATTTTACATGCGGCCAAACGGGCCCCATCAGTGCCACCCTGGTG
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                                                                              ATGACACGCCCATCAAAGGGCCCCGGGAAATCCAGCTGGAACTTGGAAATGATCACTGTC
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Qy 2324 AGAGA 2328         Db 2222 AGAAA 2226	
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OY 2204 CCAGTCTCCCATTTTAGCCCAGTGTTTCTTTGAGGACCCCTTAATCTTGCTTTCT 2283	1133 AGCCTTATCTGAGGATCAGTGATAACCGCTGTGATGTGTCCTGCTGAGAACCCTGGCTGCA 1192
2144 TATGTCGTAGAAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTCTCCCAAAC	1073 AGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGG 1132
GTCCTTAAATTTGTATAACGGTTTAATTCTGTCTTGTTCATTTTGAGTATTTTTAAAAAA	
024 TTTAGAGAATGTGTTTCAAAACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTT 	953 GTGTGAACCAGCCGGCACATACTTCTGCTCCTGCCTCCAGGCTACATCCTGCTGGATG 1012
Qy 1964 TITGCTTTTTGCGTACACAGAAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTT 2023	GCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGT 9
Qy 1906 ACTGTGTTACTGCTTTGCAAAGACCCGGGGGCTGGCGGGAACCCTGGGAGTAGCTAG 1963	TCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATG 89
QY 1847 -ATGITCAAAGACTGTGAACAGCTTGCTGTCACCTCTTCACCTCTTCCACTCCTCTCTCT	773 GAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCG 832
TTTATTTCCACTATTTCAAAGAAAATAGATTAGGTTGCGGGGGTCTGAGTCT	713 CGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATG 772
1733 AAAAAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTTCAAAGGCCTTCAG	TGGAAGGCCAGTGCTTAGACATTGATGATGATGCCCTATGGTTACTGCCAGCAGCACCTCTGTG 7
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGATACAGTTATC	AGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTC
QY 1613 GCATTTCCTGCTGAACGTTTCCCCGAAGACTCAGCCCGACTTCCTGACCTCCACCTGTA 1672	GCAACCAATGTGGAGGAGGAGGTGTGCAACAGATTCCCACCAGCAGGCAACCCACCC
CACCAAGGGACAGGAGAAGAGAGGAATTAACAGAGAGAATGAGAGCGACACAGACGTTAG	
ATGTGTCGCAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGAGCGTGCTCTCATTGG	
	AAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGA 4
	293 ATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGACATGATGTGTGTAACC 352
	233 ATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTTAG 292

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TTAGAATTTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGA
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                                                     TCATCCTTTCCTGCATCTTAGCCCAGTTTTTAC---GAAGACCCCTTAATCATGCTTTNT
                                                                       CCAGTCTCCCATTTTAGCCCAGTGTTTTTGAGGACCCCTTAATCTTGCTTTCT.
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Query Match Best Local S Matches 1841

Match 63.6%; Local Similarity 82.7%; nes 1841; Conservative

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358; DΒ

Indels Length

26;

Gaps

12;

21;

Score 1480.8; pred. No. 0; o; Mismatches

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79

GTCCCGCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCGTCTTGGACATGC

78

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RESULT 13
RAZ40029
ID AAZ40029
AC AAZ40
XX AZ40
AC AAZ40
AC Full
XX A55 E
KW Vascu
FULL
KW Vascu
KW Va
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                                                                       This sequence encodes the mouse A55 protein. The invention relates to the human A55 protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, and as cadherin/tumour metastasis inhibiting activity; tumour inhibition, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A55 protein; mouse; smooth muscle proliferation; tissue generation; wascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma; vascular endothelial thickening; had attacopoletic cell-regulator; cytokine percutaneous transluminal coronary angioplasty; blood coagulation; PTCA; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy; tumour metastasis inhibitor; ss.
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                               Page 52-55;
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RESULT 12
AAX39384
ID AAX39384
XX AAX39384
AC AAX39
AC AAX39
XX SMOOT
XX SMOOT
XX Cell
KW endot
KW myoma
KW metas
XX Mus m
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                                                       Query Match
                    Matches 1841;
                                                                                                                                         The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or remarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadohelin/tumour metastasis inhibiting activity; tumor inhibition, and as nutrient. The present sequence represents a DNA encoding the protein of the invention which can be used for modulating smooth muscle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                           Sequence
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DB; AAY56750.
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                                                                                                          GCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCACCC
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                                                     AGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCA
                                                                                                                                             AGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGG
                                                                                                                                                                                                ACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGC
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 20
P-PSDB;
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                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                 SEQ ID NO 2627; 1380pp + sequence listing; English
                          GTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCT
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         GACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAAT
                                                              ATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGC
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2000JP-0118774.
2000JP-0183765.
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Pred. No. 0;
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                                      CCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAA
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 1673; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding human extracellular/epidermal growth factor, useful for diagnosis and treatment of e.g. Marfan syndrome and wounds, also related polypeptides
                                                                                                                                                                                                                                                                                                Sequence 1720 BP; 396 A; 515 C; 434 G; 372
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                    GACCCCCTACTCAGGTCCGTACCCAGCAGCAGCTGCCCCACCACCTCTGAGCTCCAAACTATCC
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1562 1604	GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGA	1503	. OA
1502 1544	CAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCA		24 95
1442 1484	GATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGT		d Qy
1382 1424	TGGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGT	ь ь	45 50
1322 1364	CTTCCAAATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATC		pb Qy
1262 1304	CTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACAT	سر سر	5 d
1202 1244	GAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCC	1143	5 d
1142 1184	CTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCT		gg VQ
1082 1124	CTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTG	1023	dd 60
1022 1064	GCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAG		dd VQ.
962 1004	CAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCA	o o	dd Vo
902	CGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTG	<b>80</b> 80	DB 49
842 884	CCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTA		Dy Qy
782 824	TGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTG	723	pp dq VQ
722 764	GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC	705	dd Yo
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Location/Qualifiers 211..1557
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AAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAAGCCCTGGGAATGCACAGGC

CGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCGTCTTGGACATGCCAGGAATAAA

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CGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCGTCTTGGACATGCCAGGAATAAA

CCCGGCGCTCTCCCCGTGTCCTCTCCACGACTCGCTCGGCCCCTCTGGAATAAAACACCC

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Query Match Best Local S Matches 1673

cal Similarity 1673; Conserv

Conservative

71.9%; 99.8%;

Score 1674.2; Pred. No. 0; Mismatches

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Indels Length

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Gaps

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Sequence

1720 BP;

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434 G;

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other;

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This sequence encodes a novel human extracellular/epidermal growth CC factor-like protein, EEGF. This protein can be used to regulate vascular smooth muscle cell proliferation and for restoration or commencement of neurological functions diminished as a result or other CC enhancement of neurological functions diminished as a result or other CC damaging pathologies such as AIDS dementia. The protein can also be used to treat senile dementia, coular disorders such as corneal inflammation, cor targetling tumour cells, for treating kidney disorders, for liver CC regeneration or treating liver dysfunction, for treating wounds including CC all cutaneous wounds, corneal wounds, and injuries to the cepithelial-lined hollow organs of the body or resulting from trauma such as burns, abrasions and cuts as well as from surgical procedures such as csurgical incisions and skin grafting. The polypeptides can also be used CC gromote hair follicular development, to stimulate growth and cc differentiation of various epidermal and epithelial cells in vivo and in vitro and to stimulate embryogenesis. Antagonists to EEGF can be used to treat neoplasia such as cancers or tumours, skin disorders such as corneal inflammation. The products can also be used for identifying EEGF receptors, detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated extracellular/epidermal growth factor - used regulating vascular smooth muscle cell proliferation, e.g. enhancing neurological functions or treating neoplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li H,
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DB; AAW79739.
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Best Local
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
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                              CTTCCAAATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATC
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2464 GGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGAAGAGA 2509	ACCUCAGISTITICITICANGACCCCTTAATCTIGCTITCTIAGACACCCCTTAATCTTGCTTTCTTTAGACACCCCTTAATCTTGCTTTCTTT	GANAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTT		AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAATTTGTATAAC 210	GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAA 	1923 CAAAGACCCGGGACTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTTTT	AACAGCTTGCTGTCACTTCTCACCTCTTCCACTCCTCTCACTGTGTTACTGCTTTG	1803 CTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTG 1862	1743 ATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCA 1802	83 64	1623 CTGAACCTTTCCCCGAAGACTCAGCCCCGACTTCCTGACTCTCACTGTACTATTGCAGA 1682 	CAGGAGAAGAGAGAGAAATAACAGAGAGAAATGAGAGCGACACAGACGTTAGGCATTTCCTG	GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGA	CAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCGATILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1383 GATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGCTGGGACTTGGAAATGATCACTGT 1442 	1323 TGGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGT 1382 	CTTCCAAATGCAAGCCACGACCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATC

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                                                                                                         Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; didiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
                                                                                                                                                                                                                                                                            Human EGF-like
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Query Match Best Local S Matches 2224

Similarity

90.8%;

Conservative

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Pred. Score 2112.8;

ed. No. 0; Mismatches

2 20;

Gaps

DВ

Length 2509

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CGAGCTTTCTTCTCGCCTTCGCATCTCCTTCGCGCGCGTCTTGGACATGCCAGGAATAAA

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CC carrier or exciplent), a novel problemble (I) its agonist or carrier or exciplent), a novel problemble (I) its agonist or carrier or exciplent), a novel problemble (I) its agonist or carrier or exciplent), a novel problemble (I) its agonist or carrier or exciplent), a novel problemble (I) its agonist or carrier or carrier or exciplent). The products of the invention have anti-inflammatory, are used to treat immune response; or (iii) Toell and their fragments, are used to treat immune-related diseases, particularly Toell-mediated diseases. The diseases treated include contributes, systemic vasculitis, promotive expressions, rheumatoid arthritis, jurchime carrier propositis, polymyositis), cc systemic light and their fragments, are used to treat immune-related diseases, particularly Toell-mediated diseases. The diseases treated include carrier is syndrome, systemic vasculitis, sarcoidosis, carrier (I), and its (ant)agonists of disparhic inflammatory myopathies, systemic sclerosis (sclerosis (sclerosis (systemic byopathic inflammatory myopathies, systemic sclerosis, control of themolytic anemia (immune pancytopenia, paroxysmal nocturnal themolytic anemia (immune pancytopenia, paroxysmal nocturnal chemolytic almune-mediated thrombocytopenia, paroxysmal nocturnal control of themolytic systemic pancytopenia, paroxysmal nocturnal disease, control of themologial particular particular paroxysmal nocturnal disease, control of themologial particular particular paroxysmal nocturnal disease, control of themologial particular particular particular particular particular non-hepatotropic viruses), autoimmune control of active hepatitis, particular non-hepatotropic viruses), autoimmune control of active hepatitis, particular non-hepatotropic viruses), autoimmune control of active hepatitis, particular particu
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18-SEP-1997;
28-OCT-1997;
12-NOV-1997;
21-NOV-1997;
24-NOV-1997;
04-JUN-1998;
  Sequence
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                           CTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGA
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Ashkenazi AJ, Baker KP, Botstein DA, Ferrara N, Fong S, Gao W, Gerber H, Godowski PJ, Gurney AL, Kljavin IJ, Paoni NF, Roy MA, Stewart TA, Tumas

Desnoyers L, Eaton DL; Gerritsen ME, Goddard A; Mather JP, Napier MA; Par D, Watanabe CK, Williams

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cc primers for PRO polypeptides of the invention. The sequences of the climention can be used to detect the presence of a tumour in a mammal by cc comparing the level of expression of a PRO polypeptide in a test sample cc of cells from the animal and a control sample of normal cells, whereby a clipter level of expression in the test sample indicates the presence of a cc tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, cc years goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human cloud, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The CC stimulate the proliferation or differentiation of the condrovete cells. The CC proteins can be used to determine the presence of tumours and also conseptibility to tumour development, particularly adrenal, lung, colon, colorest, prostate, rectal, cervical, or liver tumours. In mammalian cc subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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18-DEC -2001

Human DNA encoding PRO polypeptide sequence #204

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disor PCR primer. 20-SEP WO200168848-A2 Homo sapiens disorder; colon;

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This is the nucleotide sequence of the human secreted protein AK647. The CC polynucleotide sequence was obtained from a human foetal kidney cDNA CC library. AK647 homologues in chicks and rodents are involved in aortic tissue development. The spatial and temporal distribution of AK647 CC indicated that it acts as an amodulator of smooth muscle cells in CC AK647 consists of multiple EGF domains. The primary structure of vasculogenesis during embryonic development. The primary structure of inducing, cytokine, cell proliferation and cell differentiation activity. CC inducing, cytokine, cell proliferation and cell differentiation activity. CC inducing, cytokine, cell proliferation and cell differentiation activity. Including severe combined immunodeficiency (SCID), HIV and other viral, bacterial and fungal infections. Regulation of immune content include a role in the regulation of haematopolesis and in the responses may also be carried out by the AK647 protein. Other uses of the protein include a role in the regulation of haematopolesis and in the creatment of uncerts and burns. CC as well as for wound healing and in the treatment of ulcerts and burns. CC ameliorating smooth muscle cell growth, vasculogenesis, restencis, can be used for preventing, treating or ameliorating smooth muscle cell growth, vasculogenesis, restencis, can be used for preventing. The proteins and tumour inhibition activity. AK647 specific contenting can be used for promoting smooth muscle cell growth or constant of ulcerts and burns. The proteins and drug screening.
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AAZ39892 standard; cDNA; 2362 ВP

AAZ39892

21-FEB-2000 (first entry)

sequence of the human secreted protein AK647.

AK647; aortic tissue development; smooth muscle cell modulator; SCID; nutritional supplement; vasculogenesis; embryonic development; infection; cytokine activity; cell proliferation; cell differentiation; detect; HIV; immune deficiency; haematopoiesis regulation; tissue regrowth; diagnose; wound healing; restenosis; atherosclerosis; drug screen; ss.

Homo sapiens

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RESULT 3
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New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential vaccines {\bf r}
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Pages 51-52; 76pp; English

The sequence is that encoding a secreted protein from a human fetal kidney clone AK647. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemastopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene

Sequence 2362 BP; 580 A; 650 C; 548 G; 584 T; 0 other;

В 20;

Length

δÃ 밁 Qy Query Match Best Local Similarity Matches 2326; Conserv 63 20 ω CCGGGCGCTCTCCCCGTGTCCTCCACGACTCGGCTCGGGCCCCTCTGGAATAAAACACCC CCCGGCGCTCTCCCCGTGTCCTCCTCCACGACTCGCTCGGCCCCTCTGGAATAAAACACCC 99.9%; Score 2326; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Mismatches ; Indels 0; Gaps 122 79

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                     ATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTTAACCAAAATGGCGG
                                              TGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCACACCCAGATCTGCAT
                                                  GACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTATCC
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Note: The open reading frame of this sequence, as well as the mature protein coding sequence are specifically claimed in claim 4.
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                                                                          TCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTAT
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## ALIGNMENTS

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XX HOMC
XX HO A55 protein; human; smooth muscle proliferation; tissue generation; vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma; vascular endothelial thickening; haematopoietic cell-regulator; cytokine; percutaneous transluminal coronary angioplasty; blood coagulation; PTCA; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy; WPI; 2000-038647/03 WO9955864-A1 Homo sapiens. Honjo T, Tashiro K, 28-APR-1998; 28-APR-1999; 04-NOV-1999. 15-FEB-2000 AAZ40027 standard; DNA; 2328 (ONOY ) ONO PHARM CO LTD. tumour metastasis inhibitor; ss. Full length human A55 protein coding sequence. (first entry) 98JP-0119731 99WO-JP02284. Nakamura T; ВP

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90464	90405 TCTTCCCAAACCCAGTCTCCTCCATTTTAGCCCAGTGTTTTCTTTGAGGACCCCTTAA 90464	90405	8
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90404	TTTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTG 90404	90345	В
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On Jun 26, 2001 this sequence version replaced gi:13509295
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Submitted (25-JUN-2001) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175210)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,G., Wincker,P., Barbtier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,G., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                             Center code: GS Web site: http:/
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Rowen, L., Madan, A., Qi
Hicks, P., James, R., Lo
Shaffer, T. and Hood, L.
                                        Unpublished
2 (bases 1
                                                          Rowen, L., Madan, A., Qin, S., Abbasi, N., Do
James, R., Loretz, C., Lasky, S., Madan, A.,
Shaffer, T. and Hood, L.
Sequencing of human chromosome 14 gene for
Trip 230, thyroid hormone receptor co-
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 171901)
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James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S., Ratt
Shaffer,T. and Hood,L.
Direct Submission
Submitted (25-APR-1999) Multimegabase Sequencing Center, U
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Apr 25, 1999 this sequence version replaced gi:4558634.
Location,Qualifiers
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Submitted (11-MAR-1999) Multimegabase of Washington, PO BOX 357730, Seattle, 3 (bases 1 to 171901)
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                       CACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGAACCCTG
                                                          GAGAGCGACACAGACGTTAGGCATTTCCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGA
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          CACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGGAGCTGGCGGGGAACCCTG
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/note="The CDNA for this gene complement(115917. 171768)
/gene="Trip230"
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae;
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Kowal, R.C., Richardson, J.A., Miano, J.M. and Olson, E.N.
Direct Submission
Submitted (25-MAR-1999) Departments of Molecular Biology and Oncology, Internal Medicine and Pathology, UT, Southwestern Center, Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235-914
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kowal, R.C., Richardson, J.A., Miano, J.M. and Olson, E.N. EVEC, a novel epidermal growth factor-like repeat-containing protein upregulated in embryonic and diseased adult vasculature Circ. Res. 84 (10), 1166-1176 (1999) 99278197
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AF137350 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	<u>.</u>	90 V		Oy Oy			Qy Db	Qy Db	Qy Db	Qy Db	Qу Db	Db .	Db	da d
AF137350 2304 bp mRNA linear ROD 18-JAN-2000 N Rattus norvegicus embryonic vascular EGF repeat-containing protein EVEC mRNA, complete cds. AF137350 AF137350.1 GI:4583508 Rattus norvegicus.	GAAGA 2326        AGA 2498	200 ACCASTICCCCITTIAGCCCASTSTITCTTEGAGACCCCTTAATCTTGCTTT 2261	TGTTCTTACAATTTGTATGAGTGTTTAACCTTTTCTCGTTCATTTTGAGTTTTT AATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAA	2022 ILLIAMAMATUTETTICAAAKCEATECCTEGTATTTCAACCATAAAGAAGTTTCAG 2081	AGTTTGCTTTTTGCGTACACAGAGAAAGGCTATGTAAACAAAC	1904 TCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCT 1961	1844 TCTATGTTCAAAGACTGTGAACAGCTTGCTGCACTTCTTCACCTCTTCCACTCCTTCTC 1903	1792 GTTTATTTCCACTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGGTCTGAG 1843	1732 CAAAAAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCA 1791	1672 ACTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGATACAGTTAT 1731	1612 GGCATTTCCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGT 1671	1552 GCACCAAGGGACAGGAGAAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGTTA 1611 		

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protein"
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secreted protein; expressed in developmental aorta, neu
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OCAL SIMILARITY 82.8%; Pred. No. 0; 19 1842; Conservative 0; Mismatches 357; Indels 113 GTCCGGCGGGGGGTTTCTTCTGGCGTTGGGATCTCCTCGCGGGGT	/codon_start. /product="dev protein" /protein_id= /protei	Diego, 9500 Gilman Drive, La Jolia, CA 92093-0613, USA Location/Qualifiers 1. 2478 /organism="Mus musculus" /db_xref="taxon:10090" 320. 1666 /note="DANCE; contains 6 cbEGF domains and 1 RGD m secreted protein; expressed in developmental acrite crest cells, balloon injured vessels, atherosclerc	Furukawa, Y., Kobuke, K., Tashiro, K. Matsumori. A., Sasayama, S., Chien, J. DANCE, a novel secreted RGD prote. atherosclerotic, and balloon inju. J. Biol. Chem. 274 (32), 22476-22. 19357779 10428823 2 (bases 1 to 2478) Nakamura, T., Yabe, D., Tashiro, K. & Direct Submitsted (09-DEC-1998) Medicine, Submitted (09-DEC-1998) Medicine,	SE S S	AF112151  N Mus musc protein	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-APR-2001) National Institutes of Headene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda,
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Contact: MGC help des
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Tissue Procurement: Lothar H
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              /db_xref="Locusid:23876"
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PAEHTSCRDQPFTILYRDMDVVSGRSVPADIFOMOATTRYPGAYYIFQIKSGNEGREF
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a 578 c 505 g 585 t
                                                                                                                                                                                        /product="fibulin 5"
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                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mammary tumor.
                                                                                                                                                                                                                                             /codon_start=1
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Matches 1673; Conserv
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1 (bases 1 to 1720)

Li,H. and Olsen,H.S.

LI,H. and Olsen,H.S.

EXTRACELULAR/EPIDERMAL GROWTH FACTOR LIKE
PAtent: WO 9846746-A 1 22-OCT-1998;

HUMAN GENOME SCIENCES INC (US); LI HAODONG
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                unidentified unidentified
396
                                                      Conservative
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211. .1557
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Pred. No. 0;
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Institute of Science, Rehovot
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/Protein_id="AAC62107.1"
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PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREF
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Accession Number U03877; possible membrane and
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Rostka,G.
Direct Submission
Submitted (05-MAR-1999) Kostka G., Down Committed (05-MAR-1999) Kostka G., Down Committed (05-MAR-1999) Kostka G., Down Committed (05-MAR)

Martinsried, GERMANY
2 (bases 1 to 2019)

Kostka,G.
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LLEQQCLDIDECRYGYQQLCANVPGSYSCTCNRGFTLNEDGRSCQDVNECATENPCV
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PAENPGCRQQFTTLYZDMDVYSGRSVVADIFOMQATTRYPGAYYIFQIKSGRBGREF
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/db_xref="taxon:9606"
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                                     TTGGCACCAAGGGACAGGAGAAGAGAGAATAACAGAGAGAATGAGAGCGACACAGACG
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HSA133490 2019 bp mRNA linear PRI 11-MAR-1999 N Homo sapiens fibulin-5. AJ133490 AJ133490.1 GI:4490529 FIBL-5 gene; fibulin-5. Homo sapiens.	98 38		1998 GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAAGGGTTTTTAGAGAATGTGTTTCAA 2057  2043 AACCATGCCTGGTATTTTCAACCATAAAGAAGTTTCAGTTGTCCTTAAATTTTGTATAAC 2102  2043 AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTTGTATAAC 2102  111111111111111111111111111111111	1923 CAAAGACCCGGGAGCTGGCGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTGCGTACACA 1982	SCTTGCTGTCACTTCTTCACCTCTTCCACTCCTTCTCACTGTGTTACTGCTTTG	1/43 ATCATTGCTCCCCTGATAGAAGATTGTTGGTGAARTTTCAAGGCCTTCAGTTCATTTCCA 1802	83 CCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGATACAGTTATCAAAAAGTATT 	1578 CAGGAGAAGAGAGGAATAACAGAGAGAATGAGAGGACACAGACGTTAGGCATTTCCTG 1637 1623 CTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGA 1682	GTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGTGCCTCTCATTGGCACCAAGGGA	ACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCA	

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cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LLHL at: http://i Series: IRAL Plate: 36 Row: n Column: 23
This clone was selected for full length sequencing passed the following selection criteria: matched mr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Contact: MGC help des
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                                                                                                                                                       /organism="Homo sapiens"
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/clone_lib="NIH_MGC_77"
/lab_host="DH10B"
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YMRQTGPISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
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303 584	Qy 243 ACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTAGATATTGATGA	Qy 183 AAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAAGCCCTGGGAATGCACAGGC	Qy 123 CGAGCTTTCTTCTCGCCTTCGCATCTCCTCGCGCGTCTTGGACATGCCAGGAATAAA	Qy 63 GCGAGCCCCGAGGGCCCAGAGGAGGACGTGCCCGAGGTCCTCCGGGGGTCCCGCCCG	TCCTCCACGACTCGCTCGGCC	Query Match 99.8%; Score 2322.8; DB 6; Length Best Local Similarity 99.9%; Pred. No. 0; Matches 2: Indels Matches 2: Indels	/or /db 622 a	JOURNAL Patent: WO 0077037-A 14 21-DEC-2000; Genentech Inc. (US) FEATURES Location/Qualifiers source 12609	Napier,M., Pan,J., Paoni,N., Ro Williams,P.M., Wood,W.I. and Zh Secreted and transmembrane poly the same	REFERENCE 1 AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerrits Goddard, A., Godowski, P., Gurney, A., Kliavin, T.T.	SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates; Catarrhini; Hominidae;	N Sequence 14 from Patent W00077037. 1 AX403659 1 AX403659.1 GI:21437116	2509	Qy 2283 GGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGAAGAGA	QY 2223 AGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTTCTTT	Qy 2163 GAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTT	Oy 2103 GGTTTAATTCTGTCTTGTTCATTTGAGTATTTTTAAAAAATATGTCGTAGAATTCCTTC
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	TLE Secreted the same URNAL Patent: W	UTHORS Baker, K.I Gurney, A Zhang, Z.	Z	)7 from Patent W00168848. GI:19170561	AX376340 2609 E	OY 2283 GGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGAAGAGA 2328		N N	2103 2316	QY 2043 AACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAAC 2102	QY 1983 GAGAAGGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAA 2042	Qy 1923 CAAAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTTGCTT	QY 1863 AACAGCTTGCTGTCACTTCTTCACCTCTTCCACTGTGTTACTGCTTTG 1922		1743 1956		1836	

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Qy 243 ACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTAGATATTGATGA 302	QY 1863 AACAGCTIGCIGTCACTTCTICACCICTTCCACTCTCTCACTGTGTTACTGCTTTG 1922
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Query Match 99.8%; Score 2324.4; DB 6; Length 2550; Best Local Similarity (100.0%; Pred. No. 0; Matches 2325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY 1563 CAGGAGAAGAGGAAATAACAGAGAGAGAGTGAGAGCGACACAGACGTTAGGCATTTCCTG 1622
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2436 AGCCCAGIGITITCTTTGAGGACCCCTTAATCTTGCTTTTGAGA	QY 1143 GAGGATCAGTGATAACCGCTGTATGTGTGCTGAGAACCCTGGCTGCAGAGAGCCAGCC
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Bandman,O., Corley.N.C. and Guegler,K.J.
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Direct Submission
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Diego, 9500 Gilman Drive, La Jolla
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                                                    GGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTAC
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ssclerotic, and balloon-injured arteries
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169
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## SUMMARIES

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## ALIGNMENTS

RESULT 1	
AF112152	
LOCUS	AF112152 2328 bp mRNA linear PRI 02-AUG-1999
DEFINITION	iens developmental arteries and neu
	protein mRNA, complete cds.
ACCESSION	AF112152
VERSION	AF112152.1 GI:5305672
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 2328)
AUTHORS	Nakamura, T., Ruiz-Lozano, P., Lindner, V., Yabe, D., Taniwaki, M.,
	Furukawa, Y., Kobuke, K., Tashiro, K., Lu, Z., Andon, N.L., Schaub, R.,

Pred. No. is the number of results predicted by chance to have a

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                ATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAG 1251
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Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
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Search completed: July 3, 2003, 17:36:03 Job time: 1988.41 secs

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BI837271
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11577 row: n column: 16
High quality sequence stop: 781.
Location/Qualifiers
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                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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National Institutes of Health, Mammalian
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     TTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTT
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                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                /note-"Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Noti; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MCC Library."
a 240 c 195 g 175 t
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/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host-"DH10B"
                                                                                                                                                                                                         43.3%;
                                                                                                                                                                                        Score 582.4;
Pred. No. 1.8e
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                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 933)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ716088 933 bp mRNA

AGENCOURT_8099803 Lupski_sympathetic_trunk

IMAGE:6190063 5', mRNA sequence.

BQ716088

BQ716088.1 GI:21854985
                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM13588 row: e column: 08
                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                quality sequence stop: Location/Qualifiers
                                                                         /db_xref="taxon:9606"
/clone="IMAGE:6190063"
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                 /tissue_type="sympathetic
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                /sex="male"
'note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                                                                                                                                 /organism="Homo sapiens"
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Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                GI:14800410
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Pred. No. 1.3e-160;
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IMAGE:5150191 5',
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hun
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5150191"
/tlissue_tvno="+umor"
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/dev_stage="7 months"
/lab_host="DH10B"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13960 row: d column: 05
High quality sequence stop: 651.
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Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 870)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
       GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTTGGATACCAGATGGAT
                                                                                                                                                                                                                                                                                                                                                                Similarity
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IMAGE:6439732 5', mRNA sequence.
                                                  TGGAACCCCTACTCGACCCCCTACTCAGGTCCCGTACCCAGCAGCGACCTGCCCACCACTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:6439732"
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/strain="FVB/N-3"
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D; Mismatches 96;
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                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENCOURT_8241132 Lupski_sympathetic_trunk
IMAGE:6187063 5', mRNA sequence.
BQ718885
BQ718885.1 GI:21857782
                                                                                                                                                                         http://image.llnl.gov
Plate: LLAM13580 row: h column:
                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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                                                                                                                                                quality sequence stop:
Location/Qualifiers
                /tissue_type="sympathetic
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                  /clone_lib="Lupski_sympathetic_trunk
                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:6187063"
                                                              /sex="male"
                                                                                                                 /organism="Homo sapiens"
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pCMV-SPORT6 (Life Technologies);
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                                                                                                                                                                                                                                                           mRNA sequence.
BI764020
BI764020.1 GI
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 880)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: pooled colon, kidney, stomach; Vector: /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NH_MGC Library."
 /db_xref="taxon:9606"
/clone="IMAGE:5183693"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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Pred. No. 3.7e-162;
0; Mismatches 4;
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REFERENCE
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11637 row: f column: 18
High quality sequence stop: 796.
Location/Qualifiers
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EST.
house mouse.
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Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri

1 (bases 1 to 796)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection
                                                 CAACCCCACAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGG
CCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5252369"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/tey_stage="7 months"
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Mammalla; Eutheria; Primate.
1 (bases 1 to 644)
Jia, L.B., Young, M.F., Touch.
Beckstrom-Sternberg, S.M., G.,
P.G., Hotchkiss, R.N. and F.
SGAP: The Skeletal Genome Au
                                                                                                                                                                                                                                                                                                                                               Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                 Intramural Sequencing Center (NISC).
Plate: 27 row: c column: 11
Seq primer: -21M13 forward primer (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Libin Jia
Medical Genetics Branch
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                                              /note="Organ: Hip; Vector: pBluescript;
Library constructed by Dr. Marian Young
Gehron Robey (NIDCR)"
195 c 154 g 149 t
                                                                                                                 /tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                    /clone_lib="Normal Human Trabecular Bone Cells"
                                                                                                                                                                                                /clone="NHTBC_cn27c11"
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/db_xref="taxon:9606"
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 Score 636;
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Yang, L.M.,

Robey

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EcoRI; Pamela

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                                                                       Contact: RODELL SILLINGS.

Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM11447 row: 1 column: 15
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wational Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                          quality sequence start: 14 quality sequence stop: 844.
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179550"
/clone_lib="NIH_MGC_115"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9508 row: d column: 01
High quality sequence stop: 675.
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/Clone_lib="NCI_CGAP_Brn64"
/Clone_lib="NCI_CGAP_Brn64"
/tissue_type="gl1oblas:coma with EGFR amplification"
/tissue_type="gl1oblas:coma with EGFR amplification"
/lab_host="DH108 [71 phage=resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Tissue Procurement: ATCC
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National Institutes of Health,
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                                          TGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATATGGAC 747
                                                                                                                    GAGTGTGCCACCGAGAAACCCCTGCGAAACCTGCGTCAACACCTACGGCTCTTTCATC 687
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 676
                                                                                                                                                                                                                                                                                         /tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: bone; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologie;
Note: this is a NIH_MCC Library."

a 227 c 210 g 181 t
                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4368227"
/clone_lib="NIH_MGC_86"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                     49.5%;
97.8%;
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Primates;
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Pred. No. 2.2e-173;
D; Mismatches 10;
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Catarrhini;
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i; Hominidae;
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                                                                                                                                                                                                                                                 Length 822;
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REFERENCE
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BM545444
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                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM12727 row: c column: 05
High quality sequence stop: 676.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5', mRNA sequence.
BM545444
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 954)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM545444 954 1
AGENCOURT_6500472 NIH_MGC_124
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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    tracking
a 278 c
           /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Noti; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:5729596"
/clone_lib="NIH_MGC_124"
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                     /tissue_type="hippocampus"
/lab_host="DH10B"
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                                                                                                       5', mRNA sequence.
BF339448
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  NIH-MGC
                                                   Homo sapiens
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http://mgc.nci.nih.gov/
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GGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCATCAACTTC
                                                                                                                                        TTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAA
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Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 891) Chordata;
Primates; Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

mRNA sapiens

CDNA

linear clone

EST 22-NOV-2000 IMAGE:4186704

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Mammalia; Eutheria; |
1 (bases 1 to 904)
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                                                              BQ716569 904 bp mRNA
AGENCOURT_8215248 Lupsk1_sympathetic_trunk
IMAGE:6187340 5', mRNA sequence.
BQ716569
BQ716569.1 GI:21855466
EST.
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         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13581 row: c column: 21
High quality sequence stop: 646.
                                                                                                                                                                                                                                                                                                                                                                                                                       h 58.9%;
Similarity 97.1%;
61; Conservative
    CCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACCAATGTGTGGATGTGGAC
                                                                                                                                                                                                           CCCGAGGCCTGCCGAGGAGACATGATGTGTGTGTAACCAAAATGGCGGGTATTTATGCATT
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                                                                                                        GAGTGTGCAACAGATTCCCACCAGTGCAACCCCAGCCAGATCTGCATCAATACTGAAGGC
                                                                                                                    CCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTCGACCCCCTACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCAGCGTCCG-3' and 5'-GACTAGTTCTAGARCGGCACCGCCCT(15)-3'. Size selected 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Bayl College of Medicine); available through Life Technologies."

Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="sympathetic
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6187340"
/clone_lib="Lupski_sympathetic_trunk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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Pred. No. 1.2e-
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GATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACC
                                                                                                                                                                                                                      TGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTTACCCTCAATGAG
                                                                                                                                                                                                                                                                ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGG
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                                                                                 TGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5752785"
/clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
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98.4%;
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Pred. No. 4.2e-229;
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Mammalla; Eutherla; Primates; Ca
1 (bases 1 to 996)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM13583 row: f column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ720516.1 GI:21859413
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 634.
Location/Qualifiers
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                                                                                       Similarity
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 TTCCAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTC
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                                                                                                                                                                 245
                                                                        Conservative
                                                                                                                                                            /note="vector: pcMv-SPORT6 (Life Technologies); Site_1
/note; Note_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGACCGGCCCT[15)-3'. Size selected in the for average insert length 1.9 kb. This is a primal library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Bay College of Medicine); available through Life Technologies."

Technologies."

284 c 242 g '224 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6188164"
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Lupski_sympathetic_trunk"
                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                   61.4%;
97.9%;
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                                                                  Score 825.4; DB 14;
Pred. No. 7.6e-218;
0; Mismatches 12;
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## ALIGNMENTS

REFERENCE AUTHORS TITLE FEATURES SOURCE ORGANISM RESULT 1 BM921371 LOCUS ACCESSION VERSION COMMENT DEFINITION KEYWORDS JOURNAL source Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM12787 row: 1 column: 10
High quality sequence stop: 738.
Location/Qualifiers Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1014)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. AGENCOURT\_6626255 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5752785 5', mRNA sequence.
BM921371
BM921371.1 GI:19371750 human. .1014

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APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Chen, Jian

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Fan, James

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION NUMBER OF SENCODING THE SAME

FILER REFERENCE: P3430R1C153

CURRENT APPLICATION NUMBER: US/10/180,552

CURRENT APPLICATION THE SAME

FILER REFERENCE: P3430R1C153

CURRENT APPLICATION THE SAME

FILE REFERENCE: P3430R1C153

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FILE REFERENCE: P3430R1C153

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FILE REFERENCE: P3430R1C153

CURRENT APPLICANT: CONTROL THE SAME

FILE REFERENCE: P3430R1 THE SAME

APPLICANT: CONTROL THE SAME

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APPLICANT: CONTROL 
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Matches 1343
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
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                                                                                                                  Query Match
Best Local Similarity
Matches 1343; Conserv
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Watanabe, Colin F
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-913-407
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C66
                                                                                 1 ATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAAGCCCCT
ATATATGTGTCGCAGTACCCATTC 1344
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Pred. No. 0;
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Prior Application removed -
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 1343; Conserv
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APPLICANT: Wood, William I.
APPLICANT: Zhong, Zemin
APPLICANT: Zhong, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
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Gurney, Austin L.
Pan, James
Smith, Victoria
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APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1086

CURRENT APPLICATION UNMBER: US/10/176,757

CURRENT FILING DATE: 2002-06-20

PTIOT APPLICATION TEMOVED - See File Wrapper of PRIOT APPLICATION TO SEE THE WITH THE 
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US-10-176-757-407
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Godowski, Paul J.
Gurney, Austin L.
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Sequence 407, Application US/10175752

Publication No. US20030022295A1

GENERAL INFORMATION:
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICATION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
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Best Local Similarity
Matches 1343; Conserv
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Godowski, Paul J
Gurney, Austin I
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; Publication No. US20030022296A1
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Prior application removed - So
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: HOMO Sapien
US-10-175-738-407
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US-10-175-738-407
; Sequence 407, Application US/10175738
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; GENERAL INFORMATION:
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APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION UMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
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Best Local Similarity
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddwrd, Audrey
APPLICANT: Godowski, Paul (
APPLICANT: Gurney, Austin I
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Semin
TITLE OF INVENTION: SECRETI
TITLE OF INVENTION: ACIDS
                                                                                                                     Sequence 407, Application US/10173706 Publication No. US20030022293A1 GENERAL INFORMATION:
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrap;
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
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US-10-175-737-407
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Best Local Similarity 99.9
Matches 1343; Conservative
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343OR1C50
CURRENT FILING DATE: 2002-06-19
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
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Gurney, Austin
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APPLICANT: Smith Victoria
APPLICANT: Smith Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I
APPLICANT: Wood, William I
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLY
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
PRIOT APPLICATION removed - See File Wrapper or Pai
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Lu
APPLICANT: Goddard, Audr
APPLICANT: Godowski, Pau
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IOR FILING DATE: 1998-11-20
IOR APPLICATION NUMBER: PCT/US98/25108
IOR APPLICATION NUMBER: PCT/US98/25190
IOR APPLICATION NUMBER: PCT/US98/25190
IOR FILING DATE: 1998-11-25
IOR FILING DATE: 1999-03-08
IOR FILING DATE: 1999-03-08
IOR APPLICATION NUMBER: PCT/US99/1225
IOR FILING DATE: 1999-06-02
IOR APPLICATION NUMBER: PCT/US99/20111
IOR APPLICATION NUMBER: PCT/US99/20111
IOR APPLICATION NUMBER: PCT/US99/2059
IOR APPLICATION NUMBER: PCT/US99/2059
IOR APPLICATION NUMBER: PCT/US99/21090
IOR FILING DATE: 1999-09-08
IOR APPLICATION NUMBER: PCT/US99/21090
IOR FILING DATE: 1999-09-15
IOR APPLICATION NUMBER: PCT/US99/21090
IOR APPLICATION NUMBER: PCT/US99/21090
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                                  ; LENGTH: 2609
; TYPE: DNA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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LENGTH: 2609
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 Query Match
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  Similarity
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Watanabe, Colin K
Wood, William I.
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Goddard, Audrey
Godowski, Paul J
Gurney, Austin L
Pan, James
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PRIOR DR APPLICATION NUMBER: 60/169495

R FILLYG DATE: 1999-12-07

DR APPLICATION NUMBER: 08/918874

DR FILLYG DATE: 1997-08-26

DR APPLICATION NUMBER: 08/933821

DR FILLYG DATE: 1997-09-19

DR APPLICATION NUMBER: 08/960507

DR FILLYG DATE: 1997-10-29

DR APPLICATION NUMBER: 09/114844

DR FILLYG DATE: 1998-07-14 OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/06840
OR FILING DATE: 1997-11-25
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR FILING DATE: 1997-12-08
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR APPLICATION NUMBER: 60/074092 OR FILING DATE: 1999-06-15

OR APPLICATION NUMBER: 60/145070

OR FILING DATE: 1999-07-20

OR FILING DATE: 1999-07-26

OR APPLICATION NUMBER: 60/145698

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OR FILING DATE: 1999-08-17 R FILING DATE: 1998-09-10
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R FILING DATE: 1998-08-10 APPLICATION NUMBER: 60/109304 FILING DATE: 1998-11-20 APPLICATION NUMBER: 60/125778 APPLICATION NUMBER: 60/100858 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/101922 FILING DATE: 1998-09-24 APPLICATION NUMBER: FILING DATE: 1997-10
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PRIOR PRIOR PRIOR PRIOR PRIOR OR FILING DATE: 2001-06-19
OR APPLICATION NUMBER: PCT/US98/14552
OR FILING DATE: 1998-07-14
OR APPLICATION NUMBER: PCT/US98/18824
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: PCT/US98/19093
OR FILING DATE: 1998-09-14
OR APPLICATION NUMBER: PCT/US98/19330
OR APPLICATION NUMBER: PCT/US98/19337
OR APPLICATION NUMBER: PCT/US98/19437 OR APPLICATION NUMBER: 09/87205
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/802706
OR FILING DATE: 2001-03-09
OR APPLICATION NUMBER: 09/808689
OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 09/866028
OR FILING DATE: 2001-05-25
OR APPLICATION NUMBER: 09/870574
OR APPLICATION NUMBER: 09/872035
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OR APPLICATION NUMBER: 09/886342 DR FILING DATE: 1999-03-03
DR APPLICATION NUMBER: 09/254460
DR FILING DATE: 1999-03-05
DR APPLICATION NUMBER: 09/254465
DR FILING DATE: 1999-03-05
DR FILING DATE: 1999-04-15
DR FILING DATE: 1999-06-14
DR APPLICATION NUMBER: 09/332928
DR FILING DATE: 1999-06-14
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DR FILING DATE: 1999-06-14
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DR FILING DATE: 1999-06-14
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DR FILING DATE: 1999-08-25
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DR FILING DATE: 1999-10-18
DR APPLICATION NUMBER: 09/423741
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APPLICATION NUMBER: 09/665350
FILING DATE: 2000-09-18
APPLICATION NUMBER: 09/709238 APPLICATION NUMBER: 09/548815 FILING DATE: 2000-04-13 APPLICATION NUMBER: 09/202088 FILING DATE: 1998-12-08 APPLICATION NUMBER: 09/180997 FILING DATE: 1998-09-10 APPLICATION NUMBER: 09/664610 APPLICATION NUMBER: 09/254311 APPLICATION NUMBER: 09 FILING DATE: 1998-08-FILING DATE: DATE: 1998-08-19 момВЕR: 09/665350 2000-09-18 2000-11-08 1998-09-09/158342 09/136828

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Query Match
Best Local Similarity
Matches 1344; Conserv
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CLONE: 45517
SEQUENCE DESCRIPTION: SE-836-561-2
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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APPLICANT: WILLIAM I. WOOD

APPLICANT: Zemin Zang
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE PO
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C7
CURRENT APPLICATION NUMBER: U$\frac{10}{066},500
CURRENT ETLING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10\frac{002}{796}
PRIOR APPLICATION NUMBER: 10\frac{002}{796}
PRIOR FILING DATE: 2001-11-15
PRIOR PPLICATION NUMBER: 60\frac{005}{2005}
PRIOR FILING DATE: 1997-08-26
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APPLICANT: Kevin I
APPLICANT: David I
APPLICANT: Luc De:
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Timothy A. Stewart
Daniel Tumas
Colin K. Watanabe
P. Mickey Williams
William I. Wood
                                                                                                                                                                                                                                  Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
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                                                                                                                                                                                                              James Pan
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Wei-Qiang Gao
Hanspeter Gerber
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Napoleone Ferrara
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David A. Botstein
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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 GAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTG
                                                                                                                  GATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACAT
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                         GATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAAC
                                                                                                      GATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACAT
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                                                    GAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTG
                                                                                                                                                        TGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAA
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Pred. No. 0;
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(Patent_No._US20020038006A1
GENERAL INFORMATION:
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                            APPLICATION NUMBER: 09/212,168
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, Olga
Corley, Neil C.
Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1386
                                                                                                                                                     APPLICATION NUMBER: US/09/836,561
FILING DATE: 16-Apr-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
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TELEFAX: 415-845-4166
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US-10-041-016-1
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Best Local S
Matches 1344
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SEQUENCE DESCRIPTION: SEQ
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION:
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                             APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                              APPLICANT:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                            ADDRESSEE: 87
STREET: 87
CITY: Cambr
STATE: MA
COUNTRY: U.
ZIP: 02140
                                                                      APPLICATION NUMBER:
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Nakamura, Tome,
NVENTION: SECRETED F
                                                                                                                                                                                    E: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                       U.S.A.
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Tashiro, Kei
Nakamura, Tomoyuki
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Lu, Zhijian
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; NAME/KEY:
; LOCATION:
US-09-275-805-1
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Best Local Similarity
Matches 1344; Conserv
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 CTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGT
                                                                    GATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGGAACCACACGTGCAAC
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US-10-041-016-1
US-10-041-016-1
Sequence 1, Application US/10041016
Patent No. US/0020165151A1
PENERAL INFORMATION:
Kenneth
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    INFORMATION FOR
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
RMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                      ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPONERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      APPLICATION NUMBER: US/10/041,016
FILING DATE: 07-Jan-2002
CLASSIFICATION: CURKNOWND
PRIOR APPLICATION DATA:
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                                                                              APPLICATION NUMBER: US/09/083,002 FILING DATE: 21-MAR-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED PROTEINS NUMBER OF SEQUENCES: 2
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
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Evans, Cheryl
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Lu, Zhijian
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Merberg, David
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Racie, Lisa A.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect_score:-
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                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                             Score
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length: 2000000000
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Match Length
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Gapop 10.0 , Gapext 1.0
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US-10-041-016-1

US-10-09-083-002-1

US-09-836-561-2

US-10-066-500-14
                US-10-066-500-14
US-10-174-590-407
US-10-175-737-407
US-10-175-737-407
US-10-175-738-407
US-10-175-738-407
US-10-175-738-407
US-10-176-752-407
US-10-176-913-407
US-10-176-913-407
US-10-180-552-407
US-10-180-552-407
US-10-13-700-407
US-10-174-572-407
US-10-174-572-407
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Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 407, Appl
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## ALIGNMENTS

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Sequence 1, Application US/09275805
CPATENT NO. US20010051358A1
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US-09-275-805-1
                                                                    TELEPHONE: (301) 309-6
TELEFAX: (301) 309-85:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLSEN, HENRIK S.
APPLICANT: LI, HAODONG
TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL
TITLE OF INVENTION: LIKE PROTEIN
NUMBER OF SEQUENCES: 11
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1717 base pairs
                                                                                                                    NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US,
FILING DATE:
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
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COUNTRY:
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TYPE: nucleic acid
STRANDEDNESS: single
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KEYWORDS
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Submitted (30-JUL-1999) Shinji Tanka, Kyushu University, Faculty Medicine, Department of Surgery II, 3-1-1 Maidashi, Higashi-ku, Fukuoka 812-9582, Japan (E-mail:shinjit@surg2.med.kyushu-u.ac.jp, Tel:81-92-642-5466, Fax:81-92-642-5482)
                                                                                                                                                                                                                                                                                                                                     Tanka, S
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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AB030655.1 GI:7328920
MBP1; mutant p53 binding
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    /product="mutant p53 binding protein 1 (MBP1)"
/protein_id="BAA92880.1"
/db_xref="f61;7328921"
/translation="MLPCTSCLPGSLLLWALLLLLGSASPQDSEEDDSYTECTDGYE
WDPDSQHCRDVNECLTIPEACKGEMKCINYGGYLCLPHSAAVINDLHGEGPPPVPP
AQHPNPCPBGYEPDDDDSCYUVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYPKIGP
BCVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCYDVNREDDMGAPCEQRCF
BCVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCYDVNREDDMGAPCEQRCF
NSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSYLCQYRCVNEPGRFSCHCPQGYQLL
                                                                                                                           /gene="MBP1"
/note="Human homologue of protein 1 (MBP1) reported 18; 3608-16, 1999)"
                                                                                                                                                                              /gene="MBP1"
97. .1428
                                                                                                                                                                                                       /organism~"Homo sapiens"
/db_xref="taxon:9606"
1. .1536
                                                                                                                  /codon_start=1
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                                                                     TACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCCATCAAAGGG
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LCREQPSSIVHRYMTITSERSVPADVFQIQATSYYPGAYNAFQIRAGNSQGDFYIRQI
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  Kostka,G.
Direct Submission
Submitted (11-FEB-1999) Kostka G.,
Max-Planck-Institut fuer Biochemie,
Martinsried, FRG
On Mar 21, 1999 this sequence versi
                                                                                                                          Giltay,R., Timpl,R. and Kostka,G. Sequence, recombinant expression and tissue localization of two novel extracellular matrix proteins, fibulin-3 and fibulin-4 matrix Biol. 18 (5), 469-480 (1999)
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1440)
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Homo sapiens mRNA for fibulin-4
AJ132819
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20068041
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FBLN4 gene; fibulin-4.
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TGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAATGT
                                                                                                                               TTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCC
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                           GAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTC
                                                                                                             TACTCCAGCTACCTCTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCAC
                                                                                                                                                                     CACCAGGGCTATGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGC
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BSYGTFLCRCHQGYELHROGFSCSDIDECSYSCTQCCVPVEPGGRESCHCPGGYQLL
ATRLQDIDECESGAHQCSEAQTCVWBHGGYRCVDTNRCCVEPY1OVSENRCLCPASNP
LCREQPSSIVHRYMTITSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQI
NVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF"
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467 c 397 g
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/product="fibulin-4"
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/db_xref="taxon:9606"
/tissue_type="melanoma"
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Kowal, R.C., Richardson, J.A.,
Direct Submission
Submitted (25-MAR-1999) Depar
                                                                Kowal, R.C., Richardson, J.A., Miano, J.M. and Olson, E.N. EVEC, a novel epidermal growth factor-like repeat-containing protein upregulated in embryonic and diseased adult vasculations. Res. 84 (10), 1166-1176 (1999)
                                                                                                                          Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia;
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                    GATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGAAACTGAGAACCCCTGTGTTCAGACC
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                                                                       TGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAG
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Dallas, 5323 Harry Hines
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YVLLEDNRSCQDINECEHRNHTCTPLQTCYNLQGGFKCIDPIVCEEPYLLIGDNRCMC
PAENTGCRDQPFTILFRDMDVVSGRSVPADIFQMQATTRYPGAYIFQIKSGNEGREF
YMRQTGFISATLVMTRPIKGPRDIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
a 620 c 550 g 595 t
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/db_xref="G1:4583509"
/db_xref="G1:4583509"
/translation="MPGLKRILTVTILALWLEHPGNAQQQCTNGFDLDRQTGQCLDID
ECRTIPEACRCDMMCVNQNGGYLCIPRTNEYVRGPYSNEYSTSYSGPYPAAAPPVPAS
NYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYW
LLEGGCLDIDECRYGYGQQLCANVPGSYSCTCNPGFTLNDDGRSCQDVNECETENPCV
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EVEC"
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/db_xref="taxon:10116"
153. .1499
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D; Mismatches 151;
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J. Biol. Chem. 2
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                                                                                    Nakamura,T., Ruiz-Lozano,P., Lindner,V., Yabe,D., Taniwaki,M Furukawa,Y., Kobuke,K., Tashiro,K., Lu,Z., Andon,N.L., Schau Matsumori,A., Sasayama,S., Chien,K.R. and Honjo,T. DANCE, a novel secreted RGD protein expressed in developing, atherosclerotic, and balloon-injured arteries atherosclerotic, and balloon-injured arteries J. Biol. Chem. 274 (32), 22476-22483 (1999)
Nakamura,T., Yabe,D., Tashiro,K.
Direct Submission
Submitted (09-DEC-1998) Medicine,
Diego, 9500 Gilman Drive, La Joll
                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                 protein mRNA,
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350. .1696
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/db_xref="GI:5305675"
                                                                                                                                                                                                                                                                                                                                                                                            /product="developmental arteries
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Nakamura,T., Ruiz-Lozano,P., Lindner,V., Yabe,D., Taniwaki,M., Furukawa,Y., Kobuke,K., Tashiro,K., Lu,Z., Andon,N.L., Schaub,R., Matsumori,A., Sasayama,S., Chien,K.R. and Honjo,T. DANCE, a novel secreted RGD protein expressed in developing, atherosclerotic, and balloon-injured arteries
J. BLO1. Chem. 274 (32), 22476-22483 (1999)
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ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGACTATTGG
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ECRTIPEACRGDMMCVNQNGGYLCIPRINPYRGPYSNYSTSYSGPYPAAAPPYPAS
NYFTISRELYCRFGYYMDDEGNGYUDUDECATDSHQCNFTQICINTEGGYTCSCTDGYW
LLEGQCLDIDECRYGYQQLCANVPGSYSCTCNFGFTLNDGRSCQDVNECETENPCV
OTCVNTYGSFICRCDPGYELEEDGIHCSDMDEGGFSEFLCDHSCWGDGSYFCSCPPG
YVLDDNRSCQDINECEHRNHTCTTSLGTCYNLOGGFKCIDPISCEPFYLLIGENRCMC
PAEHTSCEDOFFTILYRDMDVVSGRSVFADIFQWOATTRYFGAYYIFQIKSGNEGREF
VRROTGPISATLYMTRPIKGPRDIQLDLEMITVNTVINFRGSSVIRLRIYSQYPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="DANCE; contains 6 cbEGF domains and 1 RGD motif;
secreted protein; expressed in developmental aorta, neural
crest cells, balloon injured vessels, atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAD41767.1"
/db_xref="GI:5305671"
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320. .1666
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Pred. No. 8.2e-312;
0; Mismatches 144;
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                                                                                                                                                                                                                                                                                                                                             COntact: Muture Heart Hennighausen Ph.D., Robin Humph Emmail: cgppbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph Cissue Procurement: Lothar Hennighausen Ph.D., Robin Humph Cissue Procurement: Lothar Hennighausen Ph.D., Robin Humph Cissue Procured Ph.D., Robin Humph Cissue Ph.D., Robin Human Genom Conna Library Arrayed by: Baylor College of Medicine Human Genom
                                                                                                                                  Clone distribution: MGC clone distribution information can through the I.M.A.G. E. Consortium/LLNL at: http://image.llr Series: IRAK Plate: 6 Row: f Column: 8
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 6
                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Guntaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R
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Mammalia; Eutheria; Rodentia;
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Mus musculus,
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 /clone="MGC:5656 IMAGE:3482574"
/tissue_type="Mammary tumor. WA old, gross tissue."
                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
                                                                                                                       Location/Qualifiers
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clone MGC:5656
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Sciurognathi; Muridae
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                   WAP-TGF
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IMAGE:3482574, mRNA,
                                                                                                                                                                                        information can be fo http://image.llnl.gov
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                   alpha model.
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, Muzny, D.M.
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GATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACAT
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YVLLDUNRSCQDINECEHRNHTCTSLQTCYNLJGGFKCIDPISCEEPYLLIGENRCMC
PAEHTSCRDQPFTILYRDMDVYSGRSVPADIFQMQATTRYPGAYYIFQIKSGNGGFEF
YMRQTGPISATLVMTRPIKGPRDIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
3 578 c 505 g 585 t
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/db_xref="GI:13879322"
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Institute of Science, Rehovot
Location/Qualifiers
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Mammalia; Eutheria; Primates;
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         /product="UPSO"
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LLEGQCLUDIDECRYGYCQOLCANVPGSYSCTCNQFGTLNEDGRSCQDVNECATENPCV
QTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPG
YILLDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC
PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREF
YMRQTGGISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRITVSQYPF"
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                                                                                                                                        /note="50kD; similar to human S1-5 encoded Accession Number U03877; possible membrane extracellular matrix protein; urine p50 pro
                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              human.
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gurney,A.L., Pan,J.,
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Human extracellular matrix proteins
Patent: US 5872234-A 2 16-FEB-1999;
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Bandman,O., Corley,N.C. and Guegler,
Human extracellular matrix proteins
Patent: US 6303765-A 216-OCT-2001;
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AACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTAC
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 545364:
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DNA Sequen
Center, St
Web site:
Contact:
Dickson, M
R. M.
  ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGG
                                                                                          GAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCC
                                                         GAAAGCAACCAATGTGTGGATGTGGGACGAGTGTGCAACAGATTCCCACCACCAGTGCAACCCC
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http://www-shgc.stanford.edu
ltact: (Dickson, Mark) mcd@paxil.stanford.edu
kson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
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Milarity 100.
Conservative
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//product="Inknown (protein for MGC:22412)"
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LLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNRGFTLANDGRSCDVNUECATERDPCV
LLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNRGFTLANDGRSCDVNUECATERDPCV
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YILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGFFKCIDIRCEEPYLAISDNRCMC
PAENPGCRDQPFTILYBDMDVVSGRSVPADIFQMQATTRYPGAYVIFQIKSGNEGREF
YMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
88 a 650 c 547 g 582 t
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/lab_host="DH10B"
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                                                                                            CTTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTC
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Mammalia; Eutheria; P.
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Preparation: CLONTECH
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NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH Direct Submission
Submitted (Ol-FEB-2002) National Institutes of Her
Gene Collection (MCC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda, GI:18490144 Chordata;
Primates; Craniata; Vertebrata; Catarrhini; Hominidae; Health, Mammalian National Cancer da, MD 20892-2590, Euteleostomi;

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Submitted (09-DEC-1998) Medicine, University of California Diego, 9500 Gilman Drive, La Jolla, CA 92093-0613, USA Location/Qualifiers
                          Nakamura, T., Yabe, D., Direct Submission
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Nakamura, V., Rulis-le Saravan Kabasumara, V., Rulis-le Surgularra, V., Robuke, Matsumara, A., Robuke, Baraeta, a novel search of the most of the control of
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Ruils-Mozano, P., Lindner, V., Rabe, D.; Bandwaki, M., Ruils-Mozano, P., Lindner, V., Rabe, D.; Bandwaki, M., Robuke, R., Washinso, R., Lu, B., Andon, N., Li, Y. Schaub, R., Sasayama, S., Ghilen, R., Band Honjo, R., L., Sasayama, S., Ghilen, R., Band Honjo, R., L., Lie, R. Bandwaki, R. Bandwak
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ECRTIPEACRODMCVNQNGGYLCIPRUNDYNRGPYSGPYSGPYPAAAPPLSAP
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LLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCV
QTCVRTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYECSCPG
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Direct Submission
Submitted (05-MAR-1999) Kostka
Max-Planck-Institut fuer Bloche
Martinsried, GERMANY
2 (bases 1 to 2019)
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/tissue_type="melanoma"
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                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                      Location/Qualifiers
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Biochemie,
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Copyright (c) 1993 - 2003
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result a a 1344 1342.4 1342.4 1328 1113.6 1113.6 1102 372 372 372 371 371 371 371 371 312 295.8 268 260.6 260.6 260.6 250.6 345. 337. 371 369 364 363 350 347 347 882.1 227.7.6 227.7.6 227.6.6 227.6.6 227.6.6 227.6 22 2613 171901 172674 175210 1677 1677 1917 12025 2512 2512 2512 2512 2512 2512 ength 2550 2609 2609 2609 2019 1480 1561 1707 1875 1875 1875 2018 2018 1757 1825 1777 1778 1778 1358 .021 В CNS0000R CNS07EG5 AX201326 AX46184 AR095382 AF109121 AF109121 AF109121 AF093119 AF093119 AF093119 AF019122 AF019122 BC012269 AX023954 AX023954 AX023954 AX023955 AX023955 BC022280 AR036548 AR173204 AX376340 AX403659 BC031184 D89730 AJ133490 Homo sapi AF112152 Homo sapi BC022280 Homo sapi BC022280 Homo sapi AR036548 Sequence AR173204 Sequence AX403659 Sequence AX403659 Sequence AF12151 Mus muscu AF112151 Mus muscu AF112153 Rattus no AF137350 Rattus no AF109122 Mus muscu BC012269 Mus muscu AX023976 Sequence AX023954 Sequence AX023954 Sequence AX023955 Sequence AX023955 Sequence AX023955 Sequence AX023955 Sequence AX023957 Homo sap1 AX023965 Period Rattus ratt BC0131184 Mus muscu D89730 Rattus ratt BC014410 Homo sap1 AX277602 Sequence AX331116 Sequence AX331783 Sequence AX333403 Sequence AX334103 Sequence AX331103 Sequence AX33103 Sequence Description A84086 Sequence

## ALIGNMENTS

TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	A84086	RESULT 1
EXTRACELLULAK/EPIDEMAL GROWTH FACTOR LIKE PROTEIN -PEGEERER MO 98460466A 1 2250CEP1998; HUMAN GENOME SCIENGESLENGE (US)%LDG HAODONG (US)	Li,H. and Olsen,H.S.	1 (bases: 1 to 1720)	unclassified.	unidentified.	unidentified.	-	A84086.1 GI:6733224	A84086	Sequence 1 from Patent WO9846746.	A84086 1720 bp DNA		
PROTEIN										linear		
										PAT 21-JAN-2000		
										AN-2000		

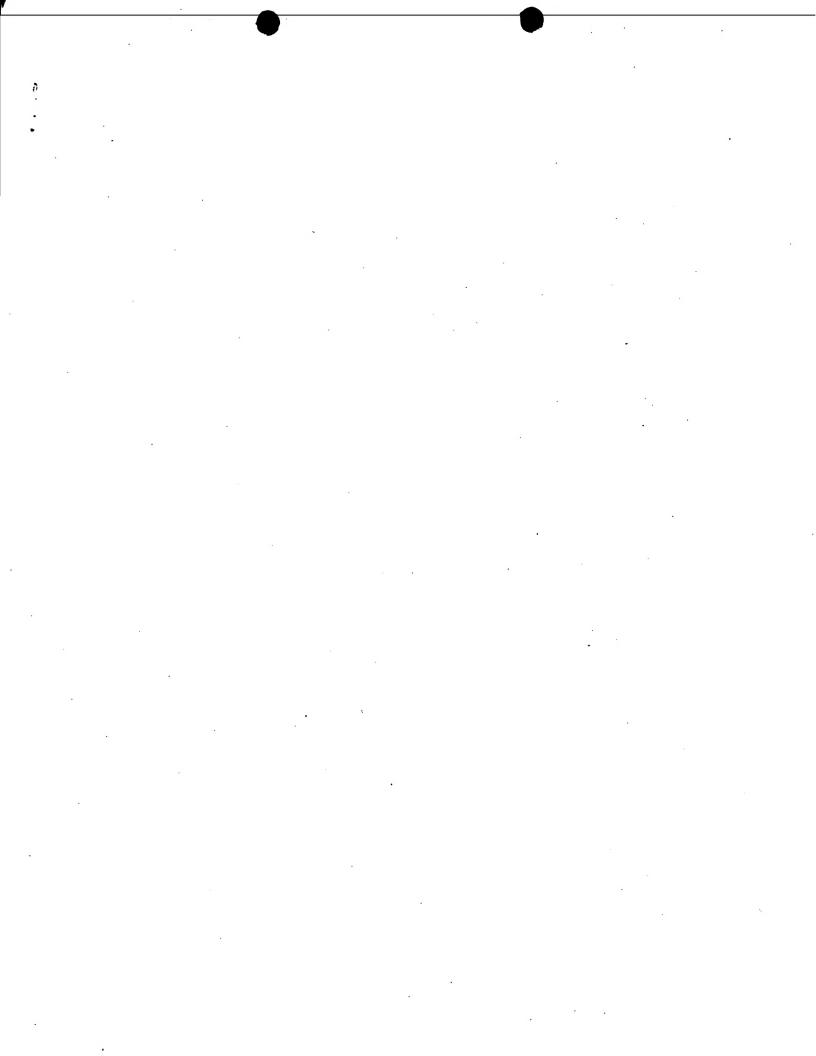
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Search completed: July 3, 2003, 17:39:59 Job time: 65.0182 secs
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; LOCATION: 1..3753
PCT-US95-02251-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 3753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 51.6; DB 5; Length 3753; Best Local Similarity 49.1%; Pred. No. 4.5e-06; Matches 166; Conservative 0; Mismatches 169; Indels 3; Gaps
                                                                                       2512 GTGGGCGGCAGGAAGTGCAAGAAAGATATAGATGAGTG 2549
                                                                                                                                                                              2452 GGTGACTGCATCAATACCAATGGTTCCTACAGATGTCTCTGTCCCCTGGGTCATCGGTTG 2511
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PCT-US95-02251-17; Sequence 17, Application PC/TUS9502251 GENERAL INFORMATION:
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     Matches
                                        Query Match
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                  FEATURE:
                                                                                                                                                MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: CE:
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                      Local
                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1994
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 Score 52.4; DB 5;
Pred. No. 3.1e-06;
0; Mismatches 241;
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PCT-US95-02251-2
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                               REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30
                  TELEPHONE:
                                                                                                                        CLASSIFICATION:
                                                                                                                                             FILING DATE:
                                                                                                                                                                              CLASSIFICATION:
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(512) 418-30
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ADDRESSEE:

E: Williams, Morgan & Amerson 7676 Hillmont, Suite 250

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US-08-479-722B-3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 934-7000
TELEFAX: (713) 934-7011
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0:
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.1
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                      GTGGGCGGCAGGAAGTGCAAGAAGATATAGATGAGTG 2552
                                                                                                           CTGGATGACAACCGAAGCTGCCAAGACATCAACGAATG 875
                                                                                                                                             GGTGACTGCATCAATACCAATGGTTCCTACAGATGTCTCTGTCCCCTGGGTCATCGGTTG
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US-08-479-722B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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LENGTH: 5499 base pair
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
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3301 GCCTGTGAAGACTTGGATGAATGTGCCTTCCCTGGAGTCTGCCCCACAGGCGTCTGCACC 3360
                                  730 CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTG 789
                                                                                                               673 TACGGCTCTTTCATCTGCCG----CTGTGACCCCAGGATATGAACTTGAGGAAGATGGCGTT 729
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                                                                          GAGGGCTCCTTCACCTGCTCAGCCTGTCAGAGCGGGTACTGGGTGAACGAAGATGGCACT
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                                                                                                                                                                                                                                                                                                                 Conservative
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NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 340
LENGTH: 220
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(220)
OTHER INFORMATION: n = A,T,C or
US-09-404-879A-340
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
Sequence 1, Application US/08282141 Patent No. 5538861
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 130; Conserv
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                                                                                                                  CCTGGCTCCTTCCGCTGCCAGNCCNAGCCGGGCTT
                                                                                                                                                                                          GAGTGTGTGGACATAGACGAGTGCCGCTACCGCTACTGCCAGCACCGCTGCGTGAACCTG
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Pred. No. 5.5e-16;
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    RESULT 12
US-08-479-722B-3
; Sequence 3, Application US/08479722B
; Patent No. 6074840
; GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Yin, Wushan
TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP)
TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 13
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Best Local Similarity 54.5%;
Matches 164; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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  CORRESPONDENCE ADDRESS
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TYPE: nucleic acid
STRANDEDNESS: unknown
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CITY: Thousand Oaks
STATE: California
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Avanzi, Giancarlo
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Pred. No. 2.7e-08;
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859 757 804

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US-08-897-443-2
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US-08-897-443-2
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   Query Match
Best Local S
Matches 211
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GENERAL INFORMATION:
                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                           TOPOLOGY: 11ne
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskette
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
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   Local Similarity hes 211; Conserv
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CITY: Palo Alto
STATE: CA
                                                                                           LIBRARY:
                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                         LENGTH: 3373 base pairs
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3174 Porter Drive
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Shah, Purvi
   Conservative
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Score 106.8; DB 2;
Pred. No. 8.9e-24;
0; Mismatches 152;
                              Length
 Indels
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                              3373;
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 Gaps
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; LOCATION: (1)...(401)
; OTHER INFORMATION: n =
US-09-643-597-278
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SOFTWARE: FastSEQ for
SEQ ID NO 278
LENGTH: 401
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                                                                                                                               Query Match
Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MCNeill, Patricia U.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/643, CURRENT FILING DATE: 2000-08-21
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                                                                                                                                                                                                                                            ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                  GCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGA
                                                   GGATGAAATGTGTTGGAATTATCATGGCGGCTTCCGTTGTTATCCACGAAATCCTTGTCA
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Fan, Ligun
Fan, Ligun
Kalos, Michael D.
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McNeill, Patricia D.
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Skeiky, Yasir A.W.
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Fanger, Gary R.
Li, Samuel X.
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54.2%;
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Pred. No. 9e-19;
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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 259
LENGTH: 1018
TYPE: DNA
ORGANISM: Human
US-09-188-930-259
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Best Local (
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wes 515; Conserv
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                                                                                                                               ACATGCGGCAAACGGGCCCCATCAAAGGGC
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                                           CCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAATTCCCTCATGAGCTACCGGG
                                                               CCCGGGAAATCCAGCTGGAACTTGGAAATGATCACTGTCAACACTGTCATCAACTTCAGAG 1297
                                                                                                                                                                             TCTACCCCGGTGCCTACAATGCCTTTCAGATCCGTGCTGGAAACTCGCAGGGGGACTTTT
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Pred. No. 2.9e-91;
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; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: STONE, EDWIN M.
APPLICANT: SHEFFIELD, VAL C.
TITLE OF INVENTION: MACULAR DEGENERATION
FILE REFERENCE: UIA-018.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 547;
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LENGTH: 2512
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Patent No. 6417342
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CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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CCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCAATAGTCTACAAATACATGAGC
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                                                   TATCCACGAAATCCTTGTCAAGATCCCTACATTCTAACACCAGAGAACCGATGTGTTTGC
                                                                                    ATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGT
                                                                                                                                                           ACAAATGA - - - ATGCCGGGAGGATGAAATGTGTTGGAATTATCATGGCGGCTTCCGTTGT
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Pred. No. 8.1e-67;
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US-08-980-514-2
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GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN S1-
TITLE OF INVENTION: EIN
NUMBER OF SEQUENCES: 3
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US-08-980-514-2
                                                                                      Matches
                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-4166
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/9 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                           LENGTH: 2018 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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617; Conserv
                   TGCCGCTTTGGATACCAGATGGATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCA 396
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                                                                                     Conservative
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61.2%;
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                                                                                Score 371.2; 1
Pred. No. 1.5e
0; Mismatches
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                                                                                2; DB 3;
1.5e-108;
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Sequence 259, Application U
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthe
                                                                                         RESULT 6
US-09-188-930-259
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Strachan, Lorna
Sleeman, Matthew
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                                                                                                                                                                           GGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCAGTACCCATTC 1344
                                                                                                                                                                                                                             CCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCATCAACTTCAGA 1296
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Olsen,
                 APPLICATION NUMBER: US/08/833,963C
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/05033
FILING DATE: 10-APR-1996
                                                                                                                                  COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            STATE:
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9410 Key West Ave
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US-08-833-963C-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1531 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
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APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Ourst, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Ski

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011cl

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEO ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 67

LENGTH: 1260

TYPE: DNA

ORGANISM: Rat

US-09-188-930-67
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Score 841.8; DB 3;
Pred. No. 2.5e-259;
5; Mismatches 102;
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CTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGT
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Query Match
Best Local Similarity
Matches 1344; Conserv
                                                                                                                                                                                                                                                                                                             STREET: 3174 POTTET Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,168

FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXT
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                              LENGTH: 2550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CORNNOTO1
CLONE: 45517
                                                                                                                                                                                            REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-833-963C-1
US-08-980-514-2
US-09-188-930-259
US-09-188-937-443-2
US-09-643-597-278
US-08-897-443-340
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PCT-US95-02251-17
              US-08-652-877-17

US-08-476-515A-17

US-08-652-877-85

US-08-652-877-89

US-08-652-877-87

US-08-652-877-87

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US-08-751-305-1
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US-08-316-650-2
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                                                       sequence 1, Appli
sequence 3, Appli
sequence 17, Appli
sequence 2, Appli
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sequence 85, Appl
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Query Match 100.0%; Score 1344; DB 2; Best Local Similarity 100.0%; Pred. No. 0;	US-08-884-072-2 US-08-884-072-2 Sequence 2, Application US/08884072 Sequence 1, Sequence 2, Neil C. APPLICANT: Gorley, Neil C. APPLICANT: Gorley, Neil C. APPLICANT: Gorley, Neil C. APPLICANT: Gorley: HUMAN EXTRACELLUIAR MATRIX PROFILE OF INVENTION: HUMAN EXTRACELLUIAR MATRIX PROFILE OF INVENTION: HUMAN EXTRACELLUIAR MATRIX PROFILE OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE OF APPLICATION SERVER OF STATE: HEAD OF WINDOWS VERSION 2.0 STATE: 4304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE COMPUTER: FASLESD for WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/884,072 FILLING DATE: HEREWITH THE SERVER OF WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/884,072 FILLING DATE: HEREWITH SERVER OF WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/884,072 FILLING DATE: HEREWITH SERVER OF WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/884,072 FILLING DATE: HEREWITH SERVER OF WINDOWS VERSION 2.0  REGISTRATION NUMBER: US/08/884,072 FILLING DATE: HEREWITH SERVER OF WINDOWS VERSION 2.0  FILLEPHONE: 415-845-4166  FILLEPHONE: 415-845-4166  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2550 base pairs INFORMATION SEQUENCE: LIBRARY: CORNNOTO1 LIBRARY: CORNNOTO1 LIBRARY: CORNNOTO1 LIBRARY: CORNNOTO1 LIBRARY: CORNNOTO1 LUBROHANDICATED LONG 45517	ALIGNMENTS	28 43.4 3.2 3546 4 US-08-872-757-3 29 41.4 3.1 .2492 4 US-09-381-779-1 30 39.8 3.0 3156 4 US-09-284-819-8 31 38 2.8 1611 4 US-09-249-697A-2 32 37.8 2.8 1611 4 US-09-363-316B-2 33 37.8 2.8 2365 4 US-09-363-316B-2 34 37.8 2.8 2365 4 US-09-363-316B-2 35 37.8 2.8 2365 4 US-09-363-316B-5 37.8 2.8 2365 4 US-09-363-316B-23 38 37.2 2.8 2365 4 US-09-363-316B-23 38 37.2 2.8 2367 4 US-08-312-870-6 41 35.4 2.6 1338 1 US-08-587-389-8 42 35.4 2.6 1338 1 US-08-587-389-8 43 35.4 2.6 1368 1 US-08-307-444A-7 44 35.4 2.6 1368 1 US-08-307-444A-7 45 35.4 2.6 1368 1 US-08-307-444A-7
Length 2550;	PROTEINS		Sequence 3, Appli Sequence 1, Appli Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 18, Appli Sequence 23, Appli Sequence 23, Appli Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli

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	1200 1274	1141 TTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATC	
, ,	1140 1214	1081 GTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCGCTACCCTGGGGCCTATTACATT	
	1080 1154	1021 TGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACGTGGTGTTCAGGACGCTCC	
	1020 1094	961 GAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTGCTGAGGAACCCTGGC 	
•	960 1034	901 CTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCCACCCCATCCGCTGT	
	900 974	841 GATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGGAACCACACGTGCAAC	
	840 914	781 GAGTGTGTAACCAGCCCGGCACATACTTCTGCTCCTGCCTCCAGGCTACATCCTGCTG	
	780 854	721 GATGGCGITCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACAT	
	720 794	661 TGCGTCAACACCTACGGCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAA	
	660 734	601 GATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACC	
	600 674	541 TGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCGTGGTTTTACCCTCAATGAG	
	540 614	481 CTTCTGGAAGGCCAGTGCTTAGACATTGATGATGTCGCTATGGTTACTGCCAGCAGCTC	
	480 554	421 ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGG	
	420 494	361 GAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCC	
	360 434	301 GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGAT	
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GGGAATGCACAGGCACAGTGCACGAATGGCTTTTGACCTGGATCGCCAGTCAGGACAGTGT

ATGCCAGGATTAAAAAGGATACTCACTGTTACCATCTTGGCACTCTGGCTTCCACATCCT ATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTTCCAAGCCCT

GGAATGCACAGCAGTGCACAAACGGCTTTGACCTGGACCGCCAGTCAGGACAGTGT

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TTAGATATTGAATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTT

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181 AACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTAC

314 240 254 Query Match Best Local S Matches 1200

Similarity

82.9%; 89.3%;

Score 1113. Pred. No. C

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2233; 0

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Conservative

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Mismatches

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This sequence encodes the mouse A55 protein. The invention relates to the human A55 protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoletic cell-regulatory activity, cytokine activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, actin/thmour metastasis inhibiting activity; tumour inhibition, and a anti-riant
                                                                                                                                                                                                                                             Novel human polypeptides myoma -
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Best Local Similarity
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                                                                                                                                                                                                                                     Sequence 2233 BP;
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                                                          GGGAATGCACAGCAGCAGTGCACAAACGGCTTTGACCTGGACCGCCAGTCAGGACAGTGT
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                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                     554 A;
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89.3%;
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                                                                                                                                                                                                                                  582 C; 510 G; 586 T; 1 other;
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                                                                                                                                                                                       Score 1113.6;
Pred. No. 0;
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RESULT 13
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DE Smoot
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Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; endothelial thickening; percutaneous transuluminal coronary angiopl myoma; hematopoietic cell-regulation; cytokine; tissue generation;
                                             Smooth muscle
                                                                                        AAZ39383
                                                                   22-FEB-2000
                                                                                                             AAZ39383 standard;
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2 CAGTACCCATTC
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                                                                  (first
                                         proliferation modulating protein coding sequence.
                                                                                                             DNA;
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generation; taxis
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Claim
                                                                                                 Novel
                                                                                                                                                                                              actin activity; chemotaxis; blood coagulation; thrombotic;
metastasis; nutrient; ss.
                                                                                                                         Honjo
                                                                                                                                   (ONOY ) ONO PHARM CO
                                                                                                                                             28-APR-1998;
                                                                                                                                                       28-APR-1999;
                                                                                                                                                                 04-NOV-1999
                                                                                                                                                                           WO9955863-A1
                                                                                                                2000-038646/03.
                                                                                                 mouse polypeptides for
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                                                                                                           AAY56750
                                                                                  Page
                                                                                                                          Tashiro
                                                                                  45-46;
                                                                                                                                             98JP-0119731
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                                                                                                                          Nakamura
                                                                                  Japanese
                                                                                                 treatment,
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                                                                                                 arteriosclerosis
                                                                                                                                                                                                   tumor; mouse
                                                                                                 and
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to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PPCA), or myoma, hematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadohelin/tumour metastasis inhibiting activity; tumor inhibition, and as nutrient. The present sequence represents the coding sequence of one protein of the invention which can be used for modulating smooth muscle cell proliferation invention provides mouse roliferation of polypeptides for treatment of diseases

Sequence 1344 BP; 325 A; 370 Ç 330 ç; 319 Ŧ; 0 other;

Matches 1200;

Conservative

Query Match Best Local Similarity

82.9%; 89.3%;

DB

21;

Length

밁 QY В δÃ 밁 δÃ 맑 Ş 멂 ρy В ρy 밁 ρ 361 361 301 301 241 241 121 181 181 121 61 61  $\vdash$ AACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTAC TTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTT GGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGT GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGAT CTAGATATTGATGAATGCCGGACCATCCCTGAGGCTTGTCGTGGGGGACATGATGTGTGTC GGGAATGCACAGCAGTGCACAAACGGCTTTGACCTGGACCGCCAGTCAGGACAGTGT GCTTCCAACTACCCCACGATTTCAAGGCCTCTTGTCTGCCGCTTTGGGTATCAGATGGAT TCAAATCCCTACTCTACATCCTACTCAGGCCCCATACCCAGCAGCGGCCCCACCAGTACCA 0; Score 1113.6; Pred. No. 0; 0; Mismatches 144; Indels 0; Gaps 420 420 360 360 300 240 180 180 120 60 300 120 0

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                                                                                                                                  vascular smooth muscle proliferation; Marfan syndrome; dementia, wound healing; alopecia; neurological disorder; ocular disorder; kidney disorder; liver disorder; embryogenesis; angiogenesis;
                                                                                                                                                                                                                               Human extracellular/epidermal
                                                                                                                therapy; ss.
                                                                                                                                                                                     Extracellular/epidermal growth factor-like protein; EEGF;
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                                                                                                                                                                                                                                                                                                                                             AAT89380 standard; cDNA;
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Location/Qualifiers 38..1216 /*tag= a
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Matches 1209;
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 CAGTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTT
                                     ATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGC
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proliferation, to treat Marfan syndrome, to stimulate wound healing, to restore normal neurological function after trauma or AIDS dementia, to treat coular disorders, to treat kidney and liver disorders, to promote hair follicular development, to stimulate growth and differentiation of epidermal and epithelial cells in vivo and in vitro, for the treatment of burns, ulcers and corneal incisions, and to stimulate embryogenesis and anglogenesis.

Nucleic acid fragments are also used as probes or primers, e.g. for dispress and dispress and anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in bacterial, insect, mammalian or plant cells. EEGF polypeptides, and polynucleotides encoding them, can be used e.g. to induce DNA synthesis, to regulate vascular smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This claimed cDNA clone codes for a human polypeptide (see AAW31705) identified on the basis of homology as a putative extracellular protein-like/epidermal growth factor-like (EEGF) protein. It was isolated from a human foetal heart cDNA library, and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding extracellular/epidermal growth protein - useful for treatment and diagnosis of e.g. neurological disease, neoplasia, psoriasis etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amplified from ATCC 97285 and the product cloned into vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 1A-D; 48pp; English.
                                                                                                                                                                                                                                       1997-512640/47.
                                                                                                                                   193 GGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTAC
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TCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACCTCTCAGCTCCAAACTAT
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(Claim 5)"
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99.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification.
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Pred. No. 0;
0; Mismatches
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08-SEP-1999
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                          Godowski PJ,
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       Zhang
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                Roy MA,
                                  J, Baker
Fong S,
                                                                                                           99US-0169495
2000WO-US00219
2000WO-US04341
2000WO-US04342
2000WO-US04414
2000WO-US05601
2000WO-US05841
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2000WO-US13358.
2000WO-US13705.
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99US-0145986.
99US-0149396.
99WO-US20111.
99WO-US20594.
99WO-US21090.
99WO-US21547.
99WO-US28313.
99WO-US28315.
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W, Gerber H,
Kljavin IJ,
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               Desnoyers L,
Gerritsen ME,
Mather JP, Nap
D, Watanabe CK
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Watanabe CK, V
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Goddard
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ams PM;
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of related
                                                                                      Claim
                                                                                                                  P-PSDB;
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                                                                                              nucleic acid molecule encoding brane polypeptide is useful for ed polypeptides -
                                                                                      Fig 9;
                                                                                      244pp; English
                                                                                                   a PRO
                                                                                                   ) polypeptide which is a therapy and identification
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present

polypeptide. The specification describes human polypeptides, designated PR0196, PR0444, PR0183. PR0185, PR02115, PR0217, PR0217, PR0242, PR0288, PR0365, PR01361, PR01308, PR01183, PR01272, PR01419, PR04999, PR07170, PR0248, PR0353, PR01318, PR01600, PR09940, PR0533, PR0301, PR0187, PR0248, PR0353, PR01318, PR01600, PR09940, PR0533, PR0301, PR06003, PR0377, PR04356, PR0246, PR0265, PR0941, PR010096, PR06003, PR0301, PR0350, PR0350, PR0350, PR0530 and PR06009, PR0910cal activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polypucleotides can also be used in gene therapy e.g. to reagents. The polynucleotides can also replace a defective gene. sequence encodes a human secreted and transmembrane

Sequence 2609 BP; 622 A; 718 C; 622 G; 647 T; 0 other;

99.9%;

Score 1342.4;

DΒ

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Length

2609

Query Match

õ 뫄 δÃ В ΩV 밁 Q Вb δÃ ₽ δÃ 밁 γQ 맑 δÃ В Ş 밁 ğ 밁 Qy Best Local Similarity Matches 1343; Conserv 481 870 421 810 690 570 510 601 361 750 301 241 181 121 450 61 ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGG AACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTAC GGGAATGCACAGGCACAGTGCAACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGT ATGCCAGGAATAAAAAGGATACTCACTGTTTACCATTCTGGCTCTCTGTCTTCCAAGCCCT GATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACC CTTCTGGAAGGCCAGTGCTTAGACATTGATGATGTCGCTATGGTTACTGCCAGCAGCTC GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTTGGATACCCAGATGGAT TCGAACCCCTACTCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCCACCACTCTCA GGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGT ATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAAGCCCT TGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAG CTTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTC ACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGG GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGAT TGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCCTCAATGAG Conservative 0; Pred. No. 0;
); Mismatches 1; Indels Gaps 180 1049 600 989 480 869 420 809 360 689 240 569 120 60 929 0

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                                                                                                                                                                                       Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
C invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC comparing the level of expression in the test sample indicates the presence of a
C higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TWR) alpha release from human
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                    Query Match
Best Local S
Matches 1343
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18-APR 2000;

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25-APR 2000;

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25-APR 2000;

25-APR 2000;

27-MAY 2000;

17-MAY 2000;

27-MAY 2000;

27-MAY 2000;

27-MAY 2000;

27-MAY 2000;

28-JUN 2000;

28-JUN 2000;

29-AUG 2000;

21-AUG 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -
                                                                                                                                                                                     Sequence
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1343; Conserv
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2000US-198585P.
2000US-199550P.
2000US-199550P.
2000US-199654P.
2000US-201516P.
                                                                                                                                      Conservative
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2000WO - US.13705.
2000WO - US.14042.
2000WO - US.14941.
2000WO - US.15264.
2000WO - US.15264.
2000WO - US.20710.
2000WO - US.2332P.
2000WO - US.3328.
2000WO - US.3328.
2000WO - US.332678.
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2000US-196820P
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atanabe CK,
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Pred. No. 0;
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anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; r cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217; RGF-11ke. se
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anti-inflammatory; anti-autoimmune; anti-diabetic;
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12-NOV-1997; 21-NOV-1997; 24-NOV-1997; 04-JUN-1998; 17-SEP-1997; 18-SEP-1997; 28-OCT-1997; Fong (GETH 17-SEP-1998; ço GENENTECH Goddard A, 97US-0059119. 97US-0059263. 97US-0063550. 97US-0065186. 97US-0066364. 97US-0066770. 98US-0088026. 98WO-US19437 Gurney ΑL, Tumas Ď

Composition containing WPI; novel polypeptide PRO245, agonist

ΣH

1; Fig 5A-1-5A-2; 177pp; English

Crarrier or excipient), a novel composition containing (apart from a containing or excipient), a novel PRO245 polypeptide (I), its agonist or cantagonist, or their fragments, for modulating: (1) infiltration of clinidammatory cells into tissue; (ii) an immune response; or (iii) T cell composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, calls into tissue; (ii) an immune response; or (iii) T cell composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, can anti-diabetic activity. (I), and its (ant)agonists cand their fragments, are used to treat immune-related diseases, decreased include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic carthritis, spondyloarthropathies, systemic sclerosis (scleroderma), cidiopathic inflammatory myopathies (dermatomyositis, polymyositis), comparative inflammatory disease, didopathic thrombocytopenia, thyroiditis, atrophic comparative menalitis, juvenile lymphocytic thyroiditis, atrophic comparative menalitis, primary biliary cirrhosis, multiple sclerosis, idiopathic demyelinating polyneuropathy, infectious hepatitis comparative hepatitis, primary biliary cirrhosis, granulomatous contentive hepatitis, primary biliary cirrhosis, granulomatous contentive mercopathy, and which mandatory bowel disease including bullous skin disease, arythema multiforme, contact dermatitis, psoriasis, combined and content dermatitis, psoriasis, and content dermatitis, psoriasis, and bullous skin disease, arythema multiforme, contact dermatitis, psoriasis,

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                      GAAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGG
                            GAAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGG
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immune disorder; human; ss.
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                                                                                                                                                                                                                          This DNA encodes a human extracellular matrix protein (ECMP)-1. cells containing a vector comprising the ECMP-1 nucleic acid are for the recombinant production of the protein. ECMP-1 and its (ant)agonists, are useful in the diagnosis, prevention, and tree of cancer and immune disorders.
                                                                                                                                                                                                                                                                                       New polynucleotide encoding extracellular matrix protein, useful in the diagnosis, prevention and treatment of immu disorders and cancer % \left( 1\right) =\left\{ 1\right\} 
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AACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTAC
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         18-MAY-1999;
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185..1532
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                                                                   'note-
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                                                                   "Secreted protein"
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580 A;

650 C;

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Score 1344; >Pred. No. 0; 0; Mismatches

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Gaps

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GCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTTGGATACCAGATGGAT

360 485 300 425

TCGAACCCCTACTCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCA

TCGAACCCCTACTCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCA

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CC polyniclectice sequence was obtained from a human foctal kidney cDNA CC library. AK647 homologues in chicks and rodents are involved in aortic tissue development. The spatial and temporal distribution of AK647 CC indicated that it acts as an a modulator of smooth muscle cells in CC vasculogenesis during embryonic development. The primary structure of EC AK647 consists of multiple EGF domains. The AK647 protein can be used as nutritional source or supplement. The protein shows both inhibitory and conditional control of inducing, cytokine, cell proliferation and cell differentiation activity. CC The protein may also be used in the treatment of immune deficiencies and cother viral, bacterial and fungal infections. Regulation of immune cc responses may also be carried out by the AK647 protein. Other uses of the protein include a role in the regulation of haematopoiesis and in the treatment of myeloid and lymphoid cell deficiencies. Uses in bone, CC cartiliage, tendon, ligament and nerve tissue regrowth are also possible, as well as for wound healing and in the treatment of ulcers and burns. CC may also have activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory, cadherin/tumour inhabition activity. AK647 specific contibodies can be used for promoting smooth muscle cell growth or vasculogenesis. The proteins and polynucleotides can also be used for detection. disgnosis and drug screening.
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  New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential vaccines  \begin{array}{c} \text{ on } & \text{ on } \\ \text{ on } & \text{ on } \\ \text{ on } & \text{ otherwise } \\ \text{ on } & \text{ otherwise } \\ \text{ otherwise } & \text{ other
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equence encodes the human A55 protein of the invention. The protein used for the treatment of diseases due to abnormal proliferation oth muscle. The polypeptides can be used according their inhibition proliferation of vascular smooth muscle cells, particularly in ng arteriosclerosis or re-narrowing by vascular endothelial
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thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity. actin/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadherin/tumour metastasis inhibiting activity tumour inhibition, and as a nutrient.

Note: The open reading frame of this sequence, as well as the mature protein coding sequence are specifically claimed in claim 4.
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clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.
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11-JAN-2000;
02-MAY-2000;
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2000JP-0118774.
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                                                               GAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human extracellular/epidermal growth useful for diagnosis and treatment of e.g. Marfan syndrome and also related polypeptides –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-121417/16.
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Query Match
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                         Score
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CDNA efficultural	AAZ61786	21	1018		316.6	45
CLONE AND	AAV86404	20	359		317	44
In EST	AAX37683	20	354	24.3		43
Succount cre	AAA14616	21	1358		337.6	42
encouring	AAA14603	21	1513		347.2	4
D SI-SECMP-I	AAZ39800	21	2018		371.2	40
dicer	AAF18229	21	1994		371.2	39
	ABK40256	24	1875		371.2	38
	AAS21402	22	1875		371.2	37
	AAC58583	21	1874	27.6	371.2	36
Human CDNA sequence	AAH13771	22	1707			ا ا
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100	AAK93463	22	670	29.0	390	30
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Secre	AAA44245	21	680	47.4		28
	AAK94129	22	1538	53.7		27
	AAK93169	22	853	53.7	721.4	26
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	AAZ61672	21	1254		843.8	21
SMOOCH MUSCLE PLOT	AAZ39388	21	1269			20
	AAZ39385	21	1269	78.6		19
	AAZ40031	21	2429	81.7		18
Smooth muscre pror	AAZ39387	21	2429		. 860	17
	AAZ39386	21	1383		098.	16
	AAZ40029	21	2233			15
Smooth muscre prot	AAZ39384	21	2233	82.9	113	14
pro	AAZ39383	21	1344	82.9		31
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Nucleotide sequenc	AAC86968	22	0		1342.4	1 5
	AAS46128	22	2609	9.9	12/2/	5

## ALIGNMENTS

RESULT 1 ABL52528 ID ABL5

ABL52528 standard; cDNA; 1347 BP

ABL52528;

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PT PT PT PT
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                                                                                                                                                                                                                                                                       Human UP50 cDNA sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                  19-JUL-2002
Artificial vascular graft for therapy of vascular diseases, has synthetic tubular element having a surface coated with endothelial,
                                                                                                       20-JUL-2000; 2000US-0620227
                                   WPI; 2002-361632/39.
                                                          Flugelman MY, Preis
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Оy	423 GACCCCCTACTCAGGTCCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTATCC 482
DЬ	692 GACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTATCC 751
у	483 CACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATG
D <sub>D</sub>	752 CACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATG
Qy	543 TGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCACCCA
В	812 TGTGGATGTGGACGAGTGTGC-AMAGATTCCCACCAGTGCAMCCCACCCAGAGTCTGCAT 870
Qy	603 CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA 662
Db	871 CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA 930
Qy	663 GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC 722
DЪ	931 GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC 990
Qy	723 TGGATCCTATTCTTGT 738
DЬ	991 TGGATCCTATTCTTGK 1006 .

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//lab_host="DHIOB"
//note="Organ: pooled pancreas and spleen; Vector:
//note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
a 240 c 195 g 175 t
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AL545549 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI015YE20 prime, mRNA sequence.
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Contact: Genoscope
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                        GTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTC
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(bases 1 to 1006)
Conservative
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/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive
a division of Invitrogen 9800 Medical Center Drive
Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
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/clone_lib="LTI_NFL006_PL2"
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 5.2e-185;
5; Mismatches 6;
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Catarrhini; Hominidae;
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Io
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Io
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Researc
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM974454 735 bp mRNA linear EST 21-MAR-2002 UI-CF-EC1-aca-j-15-0-UI.sl UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-aca-j-15-0-UI 3', mRNA sequence.
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   GTACTATTGCAGACCTGTCACCCTGCAGGACTTGCCAGCCCCCAGTTCCTATGATACAGTT
                                                                                              TAGGCATTTCCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCT
                                                                            TAGGCATTTCCTGCTGAACGTTTCCCCGGAAGAGTCAGCCCCGACTTCCTGACTCTCACCT
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(T1)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                  TAG_TISSUE-Normal Lung
and 380-383
TAG_SEQ-AAGTGCTTAC"
139 c 163 g J
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/db_xref="taxon:9606"
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/clone_l1b="UI-CF-EC1"
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Pred. No. 8e-1
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                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN11577 row: n column: 16
                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BI837271
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                        quality sequence stop:
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                              http://image.llnl.gov
http://image.llnl.gov
plate: LLAM11505 row: j column:
                                                                                                                                                                         Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 721)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                     mRNA sequence.
BI523975
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603052129F1 NIH_MGC_122 Homo
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5201767"
/clone_lib="NIH_MGC_122"
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                            GI:15348767
                                                                                                                                                                                                                                                                                                                          bp mRNA linear EST 29-AUG-2001 sapiens cDNA clone IMAGE:5201767 5',
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/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV Site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

55 a 233 c 175 g 158 t
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Length

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GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC
            GTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCC
                                                 CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA
                                                               CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA
                                                                                                                 GACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACCTCTCAGCTCCAAACTATCC
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                    GACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTATCC
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CAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCA
                                                                 GTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGGCCTACTCGAACCCCTACTC
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/dev_stage="adult, 16 yr"
/lab_host="bH10B"
/lab_host="bH10B"
/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCAGCGTCGG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
1ibrary, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
Technologies."
Technologies."
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/db_xref="taxon:9606"
/clone="IMAGE:6187063"
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Contact: Genoscope
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TCAAAAAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTC
                                                                           TACTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGATACAGTTA
                                                                                                                                    AGGCATTTCCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTG
                                      TACTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTA
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                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpoRT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CS0DI006YB07"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                            Score 723.8; DB 9;
Pred. No. 1.3e-191;
0; Mismatches 2;
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MgC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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603043221F1 NIH_MGC_116
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Plate: LLAM11458 row: 1 column:
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192
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                                                                                                                                                                                                                                             /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORP6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5183693"
/clone_lib="NIH_MGC_116"
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                                                                                                                                                                                                                                               835 bp mRNA linear EST AGENCOURT_8241132 Lupski_sympathetic_trunk Homo sapiens IMAGE:6187063 5', mRNA sequence.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
DNA Sequencing by: Agencourt Bioscience Corpo
                                                                                         1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa;
                                                                             Contact: Robert Strausberg, Ph.D
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                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13581 row: C column: 21
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 904)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                  BQ716569 904 bp mRNA
AGENCOURT_8215248 Lupski_sympathetic_trunk
IMAGE:6187340 5', mRNA sequence.
BQ716569
                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                           quality sequence stop: |
Location/Qualifiers
   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                           GAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCCGCACATAC
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Technologies."
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NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
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/lab_host="DH10B"
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/clone_lib="Lupski_sympathetic_trunk"
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Pred. No. 8.8e-211;
0; Mismatches 18;
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57; Conservative
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                                 CTTGCCAAGATGTGAACG-AGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAAC
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0; Mismatches 10;
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Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11518 row: c column:
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GTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTGCCTGCTGAGAACCCTG
                                                                                                                                                                                        ACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCT
                                                                                                                                                                                                                                                   ATGAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGC
                                                                                    GTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTG
                                                                                                                                                                     ACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCT
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 5.3e-211;
0; Mismatches 30;
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Homo sapiens cDNA clone IMAGE:5206588 5',
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Best Local Similarity
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National institutes of Health, Mammalian
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http://image.llnl.gov
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1 (bases 1 to 996)
                          GATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCCGGACAAACCCTGTGTATCG
                                                                                                                                                                                                                                                                                                                             AGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACAT
CGGATATTGGCTTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTCGCTATGGTTACTG
                                                    GTGCAACCCCACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGA
                                                                                                            CCAGATGGATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCA
                                                                                                                                        ACCACTCTCAGCTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATA
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                                                                                                                                                                                                            AGGGCCCTACTCGAACCCCTACTCGACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

284 c 242 g 224 t 1 others
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/lab_host="DH10B"
/note="Vector: pcwV-SPORT6 (Life Technologies); Sit
/note="Vector: pcwV-SPORT6 (Life Technologies); Sit
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGGACCTAGCGCGCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3' Size sele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6188164"
/clone_11b="Lupski_sympathetic_trunk"
/sex="male"
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Eutheria; Primates;
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Plate: LLAM11447 row: 1 column: High quality sequence start: 14 High quality sequence stop: 844. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 882)
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603038662F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/note="Organ: pooled brain, lung, t
pCMV-SPORT6; Site_1: NotI; Site_2:
                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179550"
/clone_lib="NIH_MGC_115"
                                            /lab_host="DH10B"
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Catarrhini;
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AL572040
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web
                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
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                                                       239
                                                                         /clone="CSODIO26YL21"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301.610 8371
Email: filang@lifetech.com URL:
bttp://filliosch.com.upc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                   http://fulllength.invitrogen.com"
184 c 208 g 220 t 2
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/db_xref="taxon:9606"
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  36.0%;
96.8%;
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No. 1.8e-223;
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5', mRNA sequence.
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                          human.
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  Metazoa;
                                                     GI:18777513
 Chordata;
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  Craniata;
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  Vertebrata;
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  Euteleostomi;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Hoscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12727 row: c column: 05
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National Institutes of Health, Mammalian
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1 (bases
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GACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATGTGAACGAGTGT
                                      TGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATATGGACGAGTGC
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(bases 1 to 954)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5729596"
/clone_lib="NIH_MGC_124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="hippocampus"
/lab_host="DH10B"
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Pred. No. 3.8e
0; Mismatches
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ismatches 6;
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Best Local Similarity 99.0
Matches 1042; Conservative
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                                                TTTTAGAGAATGTGTTTCAAAACCATGCCTGGTATTTTCAACCATAAAAGAAGTTTCAG
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Pred. No. 6.6e-281;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAM12787 row: 1 column: 10
High quality sequence stop: 738.
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AGENCOURT_6626255 NIH_MGC_115
5', mrna sequence.
BM931373
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                     GACGTGCCCGAGCTCCTCCGGGGGTCCCGCCCGCGGGGTTTCTTCTTCTCGCCTTCGCATCTC
                                  CTCCTCGCGCGTCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGC
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Location/Qualifiers
                                                                                                                                             Conservative
                                                                                                                                                                                                                                 /note="Organ: pooled brain, lung, testis; Vector: /note="Organ: pooled brain, lung, testis; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source annonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5752785"
                                                                                                                                                               40.5%;
98.4%;
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Pred. No. 3.4e-253;
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## ALIGNMENTS

VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AL571218/c COMMENT ACCESSION DEFINITION FEATURES Snoor source Li, W.B., Gruber, C., Jessee, J. and Polayes, Full-length cDNA libraries and normalizati Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France EST prime, mRNA sequence. AL571218 AL571218 AL571218 LTI\_NFL006\_PL2 Homo sapiens AL571218.1 GI:12928294 Email: seqref@genoscope.cns.fr, Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1053) /organism="Homo sapiens"
/db\_xref="taxon:9606"
/clone="CSODIO15YE20"
/clone\_lib="LTI\_NFLO06\_PL2"
/clone\_type="placenta"
/tissue\_type="placenta"
/note="Vector: pCMVSPORT 6; Site\_1: NotI;
was primed with a NotI-oligo(dT) primer Jessee, J. and Polayes, D. praries and normalization Homo 1053 bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CS0DI015YE20 3 Web : www.genoscope.cns.fr. 1st strand Five prime

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Best Local Similarity
Matches 401; Conserv
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9; Mismatches 13;
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human A55 protein.
due to abnormal pro-
used according the
 This sequence is the mouse A55 protein. The invention relates to the human A55 protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth
                                                                                                                                                                                                                                                                                  A55 protein; mouse; smooth muscle proliferation; tissue generation; vascular smooth muscle cell; arteriosclerosis; tissue reparation; mvascular endothelial thickening; haematopoletic cell-regulator; cyt percutaneous transluminal coronary angioplasty; blood coagulation; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
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RESULT 15
AAY56751
ID AAY56
XX
AC AAY56
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DT 22-FJ
XX Smoo
XX
Cell
KW endo
KW myon
KW acti
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Best Local :
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                                                                                                                                                   Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PPCA), or myoma, haematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadherin/tumour metastasis inhibiting activity; tumour inhibition, and
                                                        04-NOV-1999
    28-APR-1998;
                             28-APR-1999;
                                                                                                                                          metastasis; nutrient.
                                                                                                                                                                                                                         Smooth muscle
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                                                                                                                                                                                                                                                                                                         AAY56751
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417; Conserv
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                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              IFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMIT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYNLQGGFKCIDPISCEEPYLLIGENRCMCPAEHTSCRDQPFTILYRDMDVVSGRSVPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSDMDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLDDNRSCQDINECEHRNHTCTSLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGSYSCTCNPGFTLNDDGRSCQDVNECETENPCVQTCVNTYGSFICRCDPGYELEEDGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMILTYTILALWLPHPGNAQQQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461
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                                                                                                                                                                                                                        proliferation modulating protein mature
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    98JP-0119731
                             99WO-JP02283
                                                                                                                                                                                                                                                                                                         Protein;
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Pred. No. 1.5e-153;
0; Mismatches 17;
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                                                                                                                                                                                                                        sequence
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                                                                                                                                                                                              PTCA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364
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15-FEB-2000

(first entry)

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Matches 422;
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the mouse A55 protein. The invention relates to the human A55 protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadherin/tumour metastasis inhibiting activity; tumour inhibition, and as a nutrient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A55 protein; mouse; smooth muscle proliferation; tissue generation; vascular smooth muscle cell; arteriosclerosis; tissue reparation; m vascular endothelial thickening; membedietic cell regulator; cyt percutaneous transluminal coronary angioplasty; blood coagulation; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy; tumour metastasis inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    nutrient.
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301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human polypeptides
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                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ40029.
                                        DGVHCSDMDBCSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                   CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE
                                                                                                                                             ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
                                                                                                                                                                                                                      NQNGGYLCIPRTNPYYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD
                                                                                                                                                                                                                                                                 MPGLKRILTVTILALWLPHPGNAQQQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV
                                                                                                                                                                                                                                                                                  MPGIKRILTVTTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV
                           DGIHCSDMDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLDDNRSCQDINECEHRNHTCT
                                                                                                                                                                                                         NQNGGYLCIPRTNPVYRGPYSNPYSTSYSGPYPAAAPPVPASNYPTISRPLVCRFGYQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tashiro K,
                                                                                                                                                                                                                                                                                                                                                                                        448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 52-55; 87pp;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                          94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treatment of,
                                                                                                                                                                                                                                                                                                                                          Score 2405; DB 21;
Pred. No. 1.6e-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. arteriosclerosis
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                         448;
                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myoma;
                                                       300
                                                                                   240
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                                                                                                                                              180
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18 Ų

Matches Query Match

417;

Conservative

10;

Mismatches

Indels Length

Gaps

64

77

461; 0,

Local

Similarity

93.8%;

Score Pred.

2376; No. 1.

DB 21; l.5e-153; hes 17;

Sequence

461

A,

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RESULT 13
AAY56752
ID AAY56
XX AAY56
XX AAY56
XX AAY56
XX Call
KW endot
XW endot
XW myona
KW myona
XX W0999
YN W099
YN W09
YN W
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                                                  The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoietic cel regulatory activity, cytckine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, bic coagulation/thrombotic activity, receptor/ligand activity, cadohelin/the present sequence represents the protein of the invention which caused for modulating smooth muscle cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA; endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis; actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY56752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 54-56; 70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smooth muscle proliferation modulating protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONOY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tashiro K, Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides for treatment,
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                                                                                                                           nutrient.
                                                                                        can be
                                                                                                                                                                                        blood
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AAY56750
ID AAY56
XX AX56
XX Z2-FE
DT 22-FE
DT 22-FE
DX SMOOT
XX Cell
KW endot
KW endot
KW myoma
KW metas
XX Mus m
OS Mus m
XX XX
PN WO995
XX XX
PD 04-NC
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                          Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopolatic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
              28-APR-1999;
                                          04-NOV-1999.
                                                                      WO9955863-A1
                                                                                                 Mus musculus
                                                                                                                             metastasis; nutrient.
                                                                                                                                                                                                               Smooth muscle
                                                                                                                                                                                                                                           22-FEB-2000
                                                                                                                                                                                                                                                                      AAY56750
                                                                                                                                                                                                                                                                                                  AAY56750 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                             VPADIFQMQATTRYPGAYY IFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
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                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                               proliferation modulating protein
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                99WO-JP02283
                                                                                                                                                                                                                                                                                                   Protein;
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Pred. No. 8.1e-164;
0; Mismatches 1;
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                                                                                                                                                            taxis;
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RESULT 12
AAY54990
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AC AAY5
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standard;

Protein;

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AAY54990 AAY54990

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or remarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadohelin/theorem the present sequence represents the protein of the invention which can be used for modulating smooth muscle cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mouse polypeptides for treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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DB; AAZ39383, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 42-44;
EMITVNTVINERGSSVIRLRIYVSQYPF 448
                                                          SLQTCYNLQGGFKCIDPISCEEPYLLIGENRCMCPAEHTSCRDQPFTILY
                                                                                                        LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDYVYSGRS
                                                                                                                                        DGIHCSDMDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLDDNRSCQDINECEHRNHTCT
                                                                                                                                                    DGVHCSDMDECSFSEFLCOHECVNOPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
                                             VPADIFOMOATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRDIQLDL
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                                                                                                                                                                                                                                                                                                                                                                                    94.9%;
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                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                     Score 2405;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                            DB 21;
1.6e-155;
nes 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammallan subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                  Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183; PRO185; PRO210; PRO215; PRO217; PRO2272; PRO288; PRO365; PRO1361; PRO1308; PRO1187; PRO1972; PRO448; PRO353; PRO1318; PRO1600; PRO940; PRO333; PRO301; PRO187; PRO37; PRO4356; PRO436; PRO941; PRO1096; PRO6003; PRO6004; PRO350; PRO2630;
                                                                                                                                                                                                                                                                                                             AAB31183 standard;
Modified-site
                                                                                                                 Homo sapiens
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                                                Modified-site
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                                                                                                                                                                                                                               sequence of human polypeptide PRO210.
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                      /note=
54..57
/note-
64..70
                                                /note= "signal peptide"
21..27
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Protein;
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                                    "N-myristoylation site"
            "cell
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          attachment site"
                                                                                                                                       disorder; transgenic animal; gene therapy
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Pred. No. 8.1e-164;
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15-JUN-1999;
26-JUL-1999;
26-JUL-1999;
17-AUG-1999;
01-SEP-1999;
08-SEP-1999;
15-SEP-1999;
15-SEP-1999;
07-DEC-1999;
07-DE
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99WO-US28565.
99US-0169495.
2000WO-US00219.
2000WO-US04341.
2000WO-US04414.
2000WO-US05601.
2000WO-US05601.
2000WO-US05601.
2000WO-US05601.
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99US-0149396.
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310..316
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(GETH ) GENENTECH INC.

Paoni NF, Wood WI, Ferrara N, Godowski PJ, Ashkenaži AJ, Zhang Roy MA, Zhang Z; Fong ?ong S, Gao W, Gerbe Gurney AL, Kljavin oy MA, Stewart TA, T Baker KP, Botstein DA, W, Gerber H, Kljavin IJ, Tumas Desnoyers L, I Gerritsen ME, Mather JP, Nap S D, Watanabe CK Napier MA, Goddard ð

2001-050091/06. DB; AAC86968.

transmembrane polypeptide of related polypeptides -Isolated nucleic acid molecule encoding transmembrane polypeptide is useful for a PRO polypeptide which is a gene therapy and identification

Fig 10; 244pp; English.

polypeptide. pRO196, PRO44 PRO365, PRO13 PRO248, PRO35 PRO337, PRO14 PRO6004, PRO3 present sequence represents a human secreted and transmembrane ypeptide. The specification describes human polypeptides, designated 196, pRO444, pRO183, PRO185, pRO210, pRO215, pRO217, pRO242, pRO288, 1965, pRO1361, pRO1308, pRO1183, pRO1272, pRO1419, pRO4999, pRO7170, 1976, pRO1318, pRO1318, pRO1940, pRO933, pRO301, pRO187, pRO4941, pRO49456, pRO265, pRO941, pRO10096, pRO6003, 1937, pRO1411, pRO4956, pRO266, pRO265, pRO941, pRO10096, pRO6003, pRO10096, pRO940, pRO5003, pRO94003, pRO5003, pRO9400, pRO5003, pRO94003, pRO94003, pRO94003, pRO94003, pRO15003, pRO94003, pRO9

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DT 18-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TWR-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; co
                                                                                                                                                 18-DEC-2001
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Pred. No. 8.1e-164;
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      rectum; cervix;
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21-MAR-2000;
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2000WO-US20710
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'n ΚP, Smith Chen j 'n Watanabe CK, Wood Goddard A, Go ood WI, Zhang Godowski 2 рĮ, Gurney AL;

N-PSDB; 2001-602746/68. DB; AAS46128.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammalito screen for modulators of the compounds . mammals and

Claim 11; Fig 408; 774pp; English.

sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, catts, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate

US2001051358-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 448
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10-APR-1996;
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VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
                                                                                    LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                                                                                                                     DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                                                                                                                                        CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
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                                                   LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                                                                                     DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                                                                                                                        CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE
                                                                                                                                                                                                                                                         ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL
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RESULT 8
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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRC245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (1) infiltration of infilammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, anti-dabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune-related diseases, particularly T cell-mediated diseases. The diseases treated include particularly T cell-mediated diseases. The diseases treated include cystemic lupus erythematosus, rheumatold arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemolytic anemia (immune pancytopenia, paroxysmal nocturnal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; diopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Fong
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04-JUN-1998;
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18-SEP-1997;
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purpura immune-mediated thrombocytopenia
purpura immune-mediated thrombocytopenia), tl
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Matches 448
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                              molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota
                                                                                                                  Sequence
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genetic manipulation -
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smooth muscle cell growth, vasculogenesis, restenosis

or

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cc library. AK647 homologues in chicks and rodents are involved in aortic clisue development. The spatial and temporal distribution of AK647 consists of that it acts as an a modulator of smooth muscle cells in colorated that it acts as an a modulator of smooth muscle cells in colorated that it acts as an a modulator of smooth muscle cells in colorated that it acts as an a modulator of smooth muscle cells in colorated in a mutritional source or supplement. The primary structure of colorated in a mutritional source or supplement. The protein shows both inhibitory and cell discrete in may also be used in the treatment of immune deficiency and cell disorders, including severe combined immunodeficiency (SCID), HIV and consists include a role in the treatment of immune deficiencies and certain include a role in the regulation of haematopoiesis and in the certain include a role in the regulation of haematopoiesis and in the certain include a role in the regulation of haematopoiesis and in the certain include a role in the regulation of haematopoiesis and burns. The polynucleotides and proteins can be used for preventing, treating or ameliorating smooth muscle cell growth, vasculogenesis, restenosis, can be used for promoting and degeneration. The proteins can be used for promoting smooth muscle cell growth, catherin/tumour cellulogenesis, rand tumour inhibition activity, AK647 specific cell growth or promoting smooth muscle cell growth or catherin/tumour cellulogenesis. The proteins and polynucleotides can also be used for cell growth or catherin/tumour cellulogenesis. The proteins and polynucleotides can also be used for cellulogenesis. The proteins and polynucleotides can also be used for cellulogenesis.
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                                                                                                                                                                                                                                                                                                                    Sequence
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DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN
                                                                                                          ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
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                                        CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE
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disorders
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                    (ant)agonists, of cancer and
                            This represents a human extracellular matrix protein (ECMP)-1. Ho cells containing a vector comprising the ECMP-1 nucleic acid are for the recombinant production of the protein. ECMP-1 and its (ant)agonists, are useful in the diagnosis, prevention, and treat
                                                                              Claim 1;
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                                                                                                 polynucleotide encoding extracellular matrix protein, Evention in the diagnosis, prevention and treatment of immune orders and cancer
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DB; AAX05359.
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Best Local Sim
Matches 448;
                                                                                                   Jacobs K,
Agostino N
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                                          WPI; 2000-053298/04
N-PSDB; AAZ39892.
                                                                                                                                                                                                        19-MAY-1998;
21-MAY-1998;
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Pred. No. 3.2e-164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated extracellular/epidermal growth factor - used regulating vascular smooth muscle cell proliferation, e.g. enhancing neurological functions or treating neoplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Pred. No. 3.2e-164;
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RESULT 2
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                                                      Matches
                                                                  Query Match
Best Local
                                                                                                                                           kidney clone AK296. Such a sequence is predicted to have biological activitles which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic activity, regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding secreted human proteins - a from foetal kidney or adult retina cDNA libraries, used potential vaccines
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-095671/08.
N-PSDB; AAX07567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95709
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                     Claim 11; Pages 52-54; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; fetal kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens fetal kidney clone AK647 secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-1999
                                                                                                                                                                                                                                                                                          The sequence is that of a secreted protein from a human fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agostino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1997;
                                                                                                                                 therapy.
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                                                                 Local
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                                                      448;
                                                                 Similarity
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standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                                                                         448
                                                                                                                                                                                                                                                                                                                                                                                                                                           Racie LA,
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans C,
                                                                                                         ΑΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97us-0885610
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                                                                100.0%;
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Treacy M;
                                                   Score 2533;
Pred. No. 3.2
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie
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                                                                 3.2e-164;
                                                                                DB 20;
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                                                      Indels
                                                                               Length 448;
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                                                      Gaps
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA20000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA20001.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is greater than or equal to the score derived by analysis of the total being printed,

## SUMMARIES

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Amino acid sequenc	AAB31183	22	448	99.8	2527	10
Human PRO polypept	AAU29227	22	448	99.8	2527	9
Human EGF-like hom	AAY08063	20	448	99.8	2527	8
Human extracellula	AAU75494	23	448	100.0	2533	7
Human polypeptide,	AAM93573	22	448	100.0	2533	თ
Full length human	AAY54989	21	448	100.0	2533	ري دي
Amino acid sequenc	AAY57058	21	448	100.0	2533	4
Human extracellula	AAW94281	20	448	100.0	2533	ω
Homo sapiens fetal	AAW95709	20	448	100.0	2533	2
Human EEGF protein	AAW79739	19	448	100.0	2533	_
Description	IJ	BB	Query Match Length DB	Query	Score	Result

45	44	43	42	41	40	39	3 8	37	36	ω S	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
737	737	819	819	819	912.5	912.5	912.5	963.5	963.5	989.5	992.5	1101	1101	1106	1237.5	1282	1283	1289	1289	1289	1289	1289	1289	1289	1827	1827	1827	2230	2302	2302	2376	37	2405	40
29.1	29.1	•	•		•	•		•	38.0	•		•		•	•	50.6	•	•	•	•	•	50.9	•	•	72.1	•	•	•	•	90.9	•	93.8	94.9	94.9
683	683	451	413	413	274	274	274	387	350	295	295	493	493	201	433	443	443	443	443	443	443	443	443	443	335	335	335	392	423	423	461	461	448	448
18	12	22	23	22	23	22	21	22	20	21	21	22	22	22	21	21	22	23	2 <b>2</b>	21	21	21	20	18	23	22	21	18	21	21	21	21	21	21
AAW27600	AAR11150	AAB80440	ABG65300	AAB80391	ABB72220	AAB56020	AAY76081	AAG68188	AAY08066	AAY84708	AAY84705	AAB48077	AAB72892	AAM93220	AAB58353	AAY84706	AAB92533	AAU86130	AAU12330	AAY55850	AAY84707	AAB33418	AAY16587	AAW32110	ABB72147	AAB55947	AAY76008	$\vdash$	AAY56753	AAY56751	499	67	49	AAY56750
Human fibulin type	Fibulin C. Homo s	Gene #21 associate	Human albumin fusi	Secreted protein e	Human protein isol	Skin cell protein,	exti	ular p	Human EGF-like pro			lu	Human EFEMP1. Hom	2	Lung cancer associ	Amino acid sequenc	Human protein sequ	Human PRO226 polyp		Human S1-5 ECMP-li	A human p53 mutant	Human PRO226 prote	Extracellular prot	Human extracellula	Rat protein isolat	Skin cell protein,	Rat EGF extracellu	Human extracellula	Smooth muscle prol		Full length mouse	ת	Full length mouse	п

## ALIGNMENTS

RESULT 1 AAW79739

AAW79739 standard; Protein; 448 AA.

AAW79739;

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Key
Peptide
                                                                                                                                                                                       Extracellular/epidermal growth factor-like protein; EEGF; human; liver; vascular smooth muscle cell proliferation; neurology; pathology; AIDS; dementia; ocular; disorder; cornea; inflammation; tumour cell; kidney; wound; epithelium; surgery; skin graft; ulcer; diabetic; trophic; Marfan syndrome; treatment; hair follicle; embryogenesis; neoplasma; epidermal cell; cancer; psoriasis; detection.
                                                                                                                                                                                                                                                                       Human EEGF protein.
Region
                     Region
                                           Region
                                                                 Region
                                                                                                              Protein
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                               25-JAN-1999 (first entry)
                                                          protein"
112..153
                                                                                                   /label= signal
26..448
/label= EEGF
                      /label= EGF-1
154..190
/label= EGF-2
191..230
 /label= EGF-3
231..271
                                                                                          /note= "Extracellular/epidermal growth factor-like
                                                                                                                                                 Location/Qualifiers
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Дb	Qy	Db	Qy		Oy	ф	Qy	Ъ	Qy	Db	Qy	DЪ	Qy	Db	Qy
421	421	361	361	301	301	241	. 241	181	181	121	121	61	61		1
EMITANTVINERGSSVIRLRIYVSQYPE 448	EMITVNTVINFRGSSVIRLRIYVSQYPF 448	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLYMTRPIKGPREIQLDL 420	LQQTCXNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360	LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300	DGVHCSDMDECSFSEFICQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEE 240	_	ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180	ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180	NQNGGYLCIPRTNPYYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120		MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Search completed: July 3, 2003, 18:26:16 Job time: 89.4684 secs

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; ORGANISM: Homo Sapien
US-10-176-757-408
                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-176-913-408
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                                                                                                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Paul
APPLICANT: Gurney, Ausstin 1
APPLICANT: Pan, James
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrap;
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                 Sequence 408, Application US/10176913
                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
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                                                                                                                                                                                    Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                     Goddard, Audrey
Godowski, Paul
                                                                                                                                  Wood, William I.
                                                                                                                                                   Watanabe, Colin K.
                                                                                                                                                               Smith, Victoria
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Pred. No. 2.1e-164;
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; LENGTH: 448
; TYPE: PRT
; ORGANISM: HOMO ;
US-10-180-552-408
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US-10-180-552-408
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                                                                                       CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
           Best
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                     Query Match
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                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                 FILE REFERENCE: P3430R1C153
                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                   Zhang, Zemin
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                               Wood, William I.
                                                                                                                                                                                                          Watanabe, Colin K.
                                                                                                                                                                                                                    Smith, Victoria
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Pred. No. 2.
Score 2527; DB 9;
Pred. No. 2.1e-164;
D; Mismatches 1;
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US-10-176-482-408
US-10-176-482-408
; Sequence 408, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: BAKET, Kevin P.
; APPLICANT: Chen, Jian
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ORGANISM: Homo Sapien
-10-175-752-408
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3439R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
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                                   Desnoyers, Luc
Goddard, Audrey
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Watanabe, Colin K.
Wood, William I.
          Godowski, Paul J. Gurney, Austin'L.
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Godowski, Paul J.
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Pred. No. 2.1e-164;
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Prior Application removed - Se
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-482-408
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US-10-176-757-408
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                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Burney, Austin E
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                         Sequence 408, Appublication No.
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Best Local Similarity
Matches 447; Conserv
                                                                                                                                                                                                                             GENERAL
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I:
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1070
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
               APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
TITLE OF IN
CANT: 2hang, Zemin
OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
OF INVENTION: ACIDS ENCODING THE SAME
REFERENCE: P3430R1C86
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Godowski, Paul J.
Gurney, Austin L.
                                                              Watanabe, Colin Wood, William I.
                                                                                            Smith, Victoria
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b. US20030022297A1
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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
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US-10-173-706-408
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Matches 447; Conserv
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CURRENT FILING DATE: 2002-06-17
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Godowski, Paul J.
Gurney, Austin L.
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o. US20030022293A1
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Pred. No. 2.1e-164;
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RESULT 11
US-10-175-752-408
i; Sequence 408, Application US/10175752
; Publication No. US20030022295A1
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US-10-175-738-408
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Best Local S
Matches 447
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CURRENT FILING DATE: 2002-06-19
Prior application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
TYPE: PRT
ORGANISM: HOMO Sapien
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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                                               VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLYMTRPIKGPREIQLDL
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Watanabe, Colin K.
Wood, William I.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
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Best Local
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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10-176-758-408
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Godowski, Paul J.
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
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CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
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LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                   DGYHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
                                                                                                          CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEE
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Godowski, Paul
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Pred. No. 2.1e-164;
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APPLICATION NUMBER: PCT/US99/21090
APPLICATION 1999-09-15
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FILING DATE: 1999-09-01
APPLICATION NUMBER: PCT/US99/20594
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FILING DATE: 1998-12-01
APPLICATION NUMBER: PCT/US98/25190
FILING DATE: 1998-11-25
APPLICATION NUMBER: PCT/US99/05028
FILING DATE: 1999-03-08
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FILING DATE: 2001-03-14
APPLICATION NUMBER: 09/866028
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FILING DATE: 2001-01-22
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APPLICATION NUMBER: 09/665350
FILING DATE: 2000-09-18
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FILING DATE: 1999-11-12
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FILING DATE: 1999-10-18
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US-10-174-590-408
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US-10-174-590-408
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Best Local S
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NUMBER OF SEQ ID N
SEQ ID NO 408
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APPLICANT: Baker, Kevin
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                             APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
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TYPE: PRT
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ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL
                                Smith, Victoria Watanabe, Colin K Wood, William I.
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Godowski, Paul
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Pred. No. 2.1e-164;
0; Mismatches 1;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3130RIC7

CURRENT APPLICATION NUMBER: US/10/066,500

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 10/002,796

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/05974

PRIOR APPLICATION NUMBER: 60/05915

PRIOR APPLICATION NUMBER: 60/059115

PRIOR APPLICATION NUMBER: 60/059115

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR REPLICATION NUMBER: 60/05988

PRIOR RELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/06285

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/06286

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/06286
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US-10-066-500-15
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                              DR FILING DATE: 1997-10-27

PR APPLICATION NUMBER: 60/063733

DR FILING DATE: 1997-10-29

DR APPLICATION NUMBER: 60/066364

DR FILING DATE: 1997-11-21

DR APPLICATION NUMBER: 60/066840

DR FILING DATE: 1997-11-25

DR APPLICATION NUMBER: 60/069694

DR FILING DATE: 1997-12-16
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FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/062816 FILING DATE: 1997-10-24
                  APPLICATION NUMBER: 60/074086
   FILING
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5. US20020177165A1
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Daniel Tumas
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Hanspeter Gerber
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ennie P. Mather
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A. Botstein
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FILING DATE: 1999-03-09
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APPLICATION NUMBER: 09/254311
FILING DATE: 1999-03-03
                                                                                                                                                                                                                                                                              FILING DATE: 1998-0 APPLICATION NUMBER:
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FILING DATE: APPLICATION N
                                                APPLICATION NUMBER: 09/332929
FILING DATE: 1999-06-14
                                                                                    APPLICATION NUMBER: 09/
FILING DATE: 1999-06-14
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                                                                                                                                                                       APPLICATION NUMBER: 09/254465
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FILING DATE: 1997-08-26
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   NUMBER:
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APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08 FILING DATE: 1998-09-10 FILING DATE: 1998-02-09 1998-09-09 1998-08-18 1998-08-10 60/099803 60/099601 60/097000 60/095998

APPLICATION NUMBER: 60/099811 FILING DATE: 1998-09-10

1998-09-10 60/099812

APPLICATION NUMBER: 60/100858 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/101922 APPLICATION NUMBER: 60/109304 FILING DATE: 1998-11-20 FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/106032 60/125778

APPLICATION NUMBER: 60/139695 FILING DATE: 1999-06-15 1999-07-20 60/145698 60/145070

FILING DATE: 1999-07-26 APPLICATION NUMBER: 60/149396 FILING DATE: 1999-08-17 APPLICATION NUMBER: 60/169495 FILING DATE: 1999-12-07

1997 -09-19 08/933821 08/918874

09/136801

APPLICATION NUMBER: 09/136828 APPLICATION NUMBER: 09/136804 FILING DATE: 1998-08-19

09/158342

1998-09-10 09/202088

09/254460

APPLICATION NUMBER: 09/333075 1999-06-14 09/333077

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NAME: BROKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REGISTRATION NUMBER: 9F224

REFERENCE/DOCKET NUMBER: 9F224

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8509

TELEPAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-805-2
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RESULT 4
US-09-836-561-1
; Sequence 1, Application US/09836561
; Patent No. US20020038006A1
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Best Local Similarity 100.0%;
Matches 448; Conservative (
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PRIOR APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No. 8.
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TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
TELEX: 
    CURROWN
    INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:

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APPLICANT: Bandman,
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Corley, Neil C.
Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
ODERSTANDED SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,561
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 45517
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                ESNQCYDYDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL .180
                                                                                                                                                                                                                                          CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
            LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
                                                                                                                     CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE
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STRANDEDNESS: single
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TYPE: amino acid
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LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS
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Pred. No. 8.3e-165;
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US-09-083-002-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09083002
Patent No. US20010016650A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 448;
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                         TITLE OF INVENTION:
                                                                                                                       APPLICANT:
                                                                                                                                    APPLICANT:
                                                                                                                                                 APPLICANT:
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            COUNTRY:
                           STATE:
                                                   STREET:
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TYPE: amino acid
STRANDEDNESS: NO. US20020165151A1
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                                                 87 CambridgePark Drive
            U.S.A.
                                                                                                         Nakamura, Tomoyuki
VENTION: SECRETED PROTEINS
                                                                                                                              Honjo, Tasuku
Tashiro, Kei
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Evans, Cheryl
Agostino, Michael
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Merberg, David
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Racie, Lisa A.
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Pred. No. 8.3e-165;
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RESULT 3
US-09-275-805-2
; Sequence 2, Ap;
; Patent No. US2
; GENERAL INFOR

Sequence 2, Application US/09275805 Patent No. US20010051358A1

GENERAL INFORMATION:
APPLICANT: OLSEN, HENRIK S.
APPLICANT: LI, HAODONG

TITLE OF INVENTION:

EXTRACELLULAR
LIKE PROTEIN
11

EPIDERMAL GROWTH

CORRESPONDENCE NUMBER OF SEQUENCES:

ADDRESS:

GENOME

SCIENCES,

ADDRESSEE:

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 448 amino
TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: P-41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/083,002 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
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Pred. No. 8
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/U

2: /cgn2_6/ptodata/1/pubpaa/U

3: /cgn2_6/ptodata/1/pubpaa/U

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10 US-09-836-561-1

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10 US-10-066-500-15

10 US-10-176-758-408

10 US-10-175-737-408

10 US-10-175-737-408

10 US-10-175-738-408

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TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1251 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02251-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC009P--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
877 FTLTQDQH-----GCEEVEQP 892
                                                                              822 NTNGSYRCLCPLGHRLVGGRKCKKDIDECSQDPGLC-LPHACENLQGSYVCV----CDEG 876
                                                                                                                                                                                    264 NOPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEP 323
                                                                                                                                                                                                                                                                                                                                 644 A-KPHLCGDGGFCINFPGHYKCNCYPGYRLKASRPPICEDIDECRDPSTCPDGKCENKPG 702
                                          324 YLRISDNRCMCPAENPGCR--DOP 345
                                                                                                                                                              762 CIDVDDCEAGKVCQDGICTNTPGSFQCQCLSGYHLSRDRSRCEDIDECDFPAACIGGDCI 821
                                                                                                                                                                                                                                                                                                                                                                132 ATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ----CLDIDECR-YGYCQQ-LCANVPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                   621 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569 CVPGPSDYSCHCNAGYRSHPQHRYCVDVNECEA--EPCGPGKGICMNTGGSYNC----- 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 VYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD---ESNQCVDVDEC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEAC-RGDMMCVNQNGGYLCIPRTNP 74
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Search completed: July 3, 2003, 18:26:54 Job time: 15.8875 secs

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US-08-479-722B-2
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APPLICANT:
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, SOFTWARE: #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/0228 FILING DATE: CONCURRENTLY HEREWIT CLASSIFICATION: CTA.
                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ME
TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        COUNTRY: Un
                                                                        CLASSIFICATION:
APPLICATION NUMBER:
FILING DATE: 18-FEE
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1994
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           NAME: Parker, David L. REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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NUMBER:
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                                                                                       US 08/199,780
                                                                                                                                      us 08/316,650
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9502251 GENERAL INFORMATION:
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Best Local Similarity
Matches 119; Conserv
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LENGTH: 1833 amino aci
                                                                                    SOFTWARE: Patentin Rel
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                            ADDREET: F. STREET: HOUSTON
                                                                                                                                                                                        STALL
COUNTRY: U. 77210
                                        APPLICATION NUMBER: FILING DATE: CONCUCLASSIFICATION:
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TOPOLOGY: linear
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                                                                                                                                                                                                               United States of
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1055 PDKKGCRDVDECA--SRASCPTGLCLNTEGSFTCSACQSGYWVNEDGTACEDLDECAFPG 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1012 YVGQSGSCVDVNECLTPGICTHGRCINMEGSFRCSCEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 YCQQ-LCANVPGSYSC-TCNPGFTLNEDGRSCQDVNEC-ATENPC-VQTCVNTYGSFICR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 CDPGYELEEDGVHCSDMDECSFSEFLCQH-ECVNQPGTYFCSCPPGYILLDDNRSCQDIN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 CSNTEGSYHCECDRGYIMVRK-GHCQDINECRH-PGTC-PDGRCVNSPGSYTCL-ACEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 YRGPYS-----NPYSTP-----YSGPYPAAAPPLSAPNYPTISRPLICRFGYQM- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECEHRN-----HTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC-----PAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESNOCYDVDECATDSHOCNPTQICINTEGGYTCS-CTDGYWLLEG--QCLDIDECRY-G 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                        CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS AND COMPOSITIONS FOR STIMULATING CELLS
                                                                                                                                                           PCT/US95/02251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CVNTEGSFSCL----CETASFQPSPDSGECLDIDECEDRED
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Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                         America
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                                                                                                                                                                                                                                                      Version
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US-08-897-443-1
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   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOTTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: UTRSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Por CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-845-4166
                                                                                                                                                                          UTRSNOT02
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Score 475; DB 2; Pred. No. 5.4e-30;
                            Length 638;
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US-08-479-722B-2
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                                    TELEFAX: (713)
INFORMATION FOR SEQ
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-FEB-
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                               REFERENCE/DOCKET NUMBER: 4100.000500/FUS TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PRILING DATE: 21-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: LATENT TGF( BINDING TITLE OF INVENTION: GENES, COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US,
                                                                  TELEPHONE:
                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1994
                                                                                                                  NAME: Fussey, Shelley REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
   LENGTH:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/479,722B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 CRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRV 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 DECSFSEFICQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 SNHGCQ--HECVNTDDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNMEESYY 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 DSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDECRYGY--CQQLCANVPGSYS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 LCVNVPGSFVCQCYSGYALAEDGKRCVAVDYCASENHGCEHE--CVNADGSYLC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 VYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 LCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGFKCIDPIRCEEPYLRISDNR-C----MCPAENPGC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGC--EHSCVSS 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas
1833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7676 Hillmont,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonadio, Jeffrey
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                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams, Morgan & Amerson
76 Hillmont, Suite 250
                                                                   (713) 934-7000
                                                                                                                                                                        18-FEB-1994
                                    934-7011
ID NO: :
                                                                                                                                                                                    US 08/199,780
                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version
                                                                                                             39,458
                                                                                                                                                                                                                                     US 08/316,650
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                                                  RESULT 10
US-09-188-930-336
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GENERAL
                 Sequence 336, Application Patent No. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.0%;
Best Local Similarity 48.3%;
Matches 171; Conservative 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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LIBRARY: GE...
CNE: 458228
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 INFORMATION:
                                                                                                                      334
                                                                                                                                                        395
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                                                                                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                                                                                             156 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE
                                                                                                                                                                                                                                                                                                                                                215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC
                                                                                                                                                                                                                                                                                                                                                                                                  96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 APPLSAPNYPTISRPLICREGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC
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                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                           PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
                                                                                                                                                     RQTGPISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
                                                                                                                                                                                       PVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL
                                                                                                                                                                                                                                                                                                                            NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP
                                                                                                                    RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
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                                   US/09188930A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 963.5; DB 4;
; Pred. No. 5.8e-69;
55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0333
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95

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APPLICANT: Watson, James D.
APPLICANT: Steeman, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: And Methods For Their Use
FILE REFERENCE: 11000,1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 336
LENGTH: 274
TYPE: PRT
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5177197-30
; Patent No.
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PACENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
SEQ ID NO:30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.0%; Score 912.5; DB 4; Best Local Similarity 56.0%; Pred. No. 4.3e-65; Matches 154; Conservative 47; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1394
615 -----CPAGFMASEEGTNCIDVDECLRPDVCGEGHCVNTVGAFRCEYCDSGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SGAHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNPLCREQPSSIVHRYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                        128;
                                                                                                                                                                                                                                                                                                                                                       16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
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                                                                                                                                                                                                      YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLI-----
                                                                                                                                                                                                                                                                           CINLPURYTCICYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSFLCI-----
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; Pred. No. 4.3e-35;
52; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1394;
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US-08-980-514-3
                                                                                                                                        Patent No.
                                                                                                                                                       Sequence 3, Application US/08980514
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Best Local :
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                                                                                                                   GENERAL INFORMATION:
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                              APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN STITLE OF INVENTION: EIN
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,963C
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy disk
                NUMBER OF SEQUENCES:
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Local Similarity 48.3%;
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                                                                                                                                                                                                                                            RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
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Pred. No. 5.8
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GENERAL INFORMATION:

APPLICANT:
APPLICANT:

APPLICANT: Guegler, ITLE OF INVENTION:

Bandman, Olga
Corley, Neil C.
Guegler, Karl J.
VENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

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US-09-212-168-5
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US-08-980-514-3
Sequence 5, Application Patent No. 6303765
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Best Local !
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INFORMATION FOR SEQ ID NO:
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LIBRARY: GenBa
CLONE: 458228
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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MEDIUM TYPE: Diskette
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LENGTH: 387 amino acids
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RESULT 6
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                                                                                                              GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX
NUMBER OF SEQUENCES: 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LIBRARY: BRSTNOT13
CLONE: 2786449
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                          CORRESPONDENCE ADDRESS
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 STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                         356 VSGRSVPADIFOMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRE 415
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                     CA
                                                       E: Incyte Pharmaceuticals, 3174 Porter Drive
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                                                                                                                                  PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET:
                   ADDRESSEE:
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RESULT 7
US-08-833-963C-9
; Sequence 9, Application US/08833963C
; Patent No. 5916769
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; LIBRARY: GenBa
; CLONE: 458228
US-08-884-072-5
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GENERAL INFORMATION:
APPLICANT: Olsen, et al.
TITLE OF INVENTION: Extri
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NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Herewith CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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OPERATING SYSTEM:
SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 38.0%; Score 963.5; DB 2; Similarity 48.3%; Pred. No. 5.8e-69;
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RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
                                                                                                                                                                                                                                                                                                                                            PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM
                                                                                                                                                                                                                                                                                                                                                                                                           QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP
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         HCABA58X
                           Extracellular/Epidermal Growth
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155 95

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S: Human Genome Sciences, 9410 Key West Ave

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US-08-833-963C-2
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                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PStentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,963C

FILING DATE: 11-APR-1997

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Olsen, et al.
TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
TITLE OF INVENTION: HCABA58X
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (167)...(167)
NAME/KEY: UNSURE
LOCATION: (183)...(183)
                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/05033
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (166)...(166)
NAME/KEY: UNSURE
TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                   STREET: 9410 Key
CITY: Rockville
STATE: MD
COUNTRY: USA
                     REFERENCE/DOCKET NUMBER: PF
                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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93.7%;
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Pred. No. 1.2e-134;
6; Mismatches 15;
                                                                                                                                                                                         Version
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
TOPOLLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Local Similarity 49.98;
411 YVLDLEMVIMNSLMSYRASSVLRLTVFVGAYTF
                   416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
                                                                     351
                                                                              356 VSGRSVFADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGFISATLVMTRPIKGPRE 415
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                                                                                                                              291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNPLCREQPSSIVHRYMTI
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                                                          TSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTGPRE
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                                                                                                                                                                                                                              YELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR
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                                                                                                                                                                                                                                                                                                                                                                                                EMKCINHYGGYLCLPRSAAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP 111
                                                                                                                                                          NHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDV 355
                                                                                                                                                                                                                                                              YCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG
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443
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US-08-980-514-1
                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08980514
Patent No. 6004753
GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
              APPLICATION NUMBER: US/08/91 FILING DATE: Filed Herewith
                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                          STREET: 3174 PO
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                          3: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                                                           USA
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                               US/08/980,514
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US-09-212-168-1
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                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/884,072
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
        INFORMATION
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                         TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                          TELEX:
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        FOR SEQ
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Corley, Neil C.
                                       415-845-4166
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                                                                                                                              APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated Fro
TITLE OF INVENTION: And Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 186
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US-09-188-930-186
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 186,
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Best Local Similarity
FEATURE:
NAME/KEY: UNSURE
LOCATION: (14)...(124)
NAME/KEY: UNSURE
LOCATION: (135)...(135)
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IMMEDIATE SOURCE:
LIBRARY: CORNNOTO1
CLONE: 45517
9-212-168-1
                                                                                                         LENGTH: 337
TYPE: PRT
                                                                                        ORGANISM: Rat
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Pred. No. 2.6e-193;
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Use
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240 240 180 180 120 60

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                 963.5
963.5
963.5
963.5
912.5
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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PCT-US95-02251-3
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US-08-316-500-3
US-08-479-7228-4
US-08-897-443-3
US-08-110-116-3
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US-08-08-185-432-16
US-08-08-185-232-1
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US-08-832-384-19
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US-08-832-384-19
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US-08-980-514-1
US-08-884-072-5
US-08-8890-514-3
US-08-980-514-3
US-09-212-188-5
US-09-188-930-336
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      Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 3, Appli
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Sequence 36, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 19, Appli
Sequence 34, Appli
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US-08-884-072-1
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ω	2, A	17	Sequence 3, Appli	Sequence 18, Appl	20,	Sequence 20, Appl	2		19,	1	37,	•	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 34, Appl	Sequence 34, Appl

## ALIGNMENTS

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; LIBRARY: COR
; CLONE: 45517
US-08-884-072-1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSSQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,072
FILING DATE: Herewith
CLASSIFICATION 124
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandmau, ~_,
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                       TYPE: amino aci
STRANDEDNESS: s
TOPOLOGY: linea
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 POIT CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                  LENGTH:
                                                                                                                                                                amino acid
                                                                                                                                                                              448 amino acids
                                                                                                                            SS: single
linear
100.0%;
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Pred. No. 2.6e-193
                 Length
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785

PIECNPGYTLGSDDKCVDIDECQKQNGGCS--HRCSNTEGSFKC----SCPPGYELDSDQ 838

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RESULT 15
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Best Local 9
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PROSITE; PS00268; CECROPIN; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_3.
PROSITE; PS01187; EGF_CA; UNKNOWN_8.
PROSITE; PS50092; TSP1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Partial sequence of fibulin-6 with a c-terminal region domain II and III of the fibulin family."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ306906; CAC37630.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam; PF00047; 19; 17.
Pfam; PF00090; tsp_1; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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2455 KTCPEGSEASHDTCVDIDECENTD-ACQHECKNTFGSYQCICPPGYQLTHNGKTCQDIDE
                                                                                                                                                                              2275 NVCRPDQHCKNTRGGYKCIDLCPNGMTKAENGTCIDIDECKDGTHQCRYNQICENTRGSY
                                                                                                                                                                                                                                         2219 FRRT-SDGLSCQDINECQESSPCHQRCFNAIGSFHCGCEPGYQL-KGRKCMDVNECR--Q
                                                                                                                                                    189
                               247
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                                                                                                                                                                                              136 HQCNPTQICINTEGGYTC--SCTDGYWLLE-GQCLDIDECRYGYCQ----QLCANVPGSY 188
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                                                                                                                                                                                                                                                                     76 YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDS 135
                                                                                                                                                                                                                                                                                                                                  16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
                                                                                                                                    SCTCNPGFTLNEDGRSCQDVNEC-ATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCS- 246
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                                                                                                                   RCVCPRGYRSQGVGRPCMDINECEQVPKPCAHQCSNTPGSFKCICPPGQHLLGDGKSCAG
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ilarity 26.9%;
Conservative 6
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TSP1.
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                 -DMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINE 291
                                                                                                                                                                                                                                                                                                                                                             ; Score 548; DB 4; Length 2673; ; Pred. No. 7.4e-46; 66; Mismatches 203; Indels 122;
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                                                                                                                                                                                       292 CEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRIS-DNRCM--CPAENPGCRDQPFTI 348
----LKGVVYTTRPLREAETYRMRVRASSYSANGTIEYQTTFIV--YIAVSAYPY 2673
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Search completed: July 3, 2003, 18:21:57 Job time : 35.9041 secs

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RESULT
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01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-JUN-2002 (TrEMBLrel. 21, L
CG7526 protein (Fragment).
CG7526
          MEDININ-BURNELLY
MEDININ-20196006; PubMed-10731132;

MEDININ-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Barendale J., Bayraktaroglu L., Beasley E.M.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                         STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECVNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDVDECNLGSHDCGPLYQCRNTQGSYRCDAKKCGDGELQNPMTGEYIDECVTGHNCGAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATLMDDCLESQRCLNTPGSFKCIRTLSCGTGYAMDSETERNNCFLIILNNTFNCKYFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ESAPNYPTISRPLICREGYQMD---ESNQCV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --IP---RTNPVYRGP---YSNPYSTPYSGPYPAAAPP---
В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DVDECATDSHQCNPTQICINTEGGYTCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
S., Dahlke C.,
er A., Deng Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CMCPAENPGCRDQPFTILYRDMDVVSGRSVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CTDGYWL--LEGQCLDIDECRYGYCQQL-CANVPGSYSCTCNP
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
 Mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1394
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                  607
                                                                                                                                                                                                                                                                                          507
                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                       DMDECS-FSEFICQHECVNQPGTYFCSCPPGYILLDDNRSCQ
                                                                                                                       YSCTCNPGFTLNEDGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCS
                                                                                                                                                                  SLANGNC--SHFCQNEPGGFQCACPLGYALSEDMRTCQDIDECLDSNGQCSQLCLNQPGG
                                                                                                                                                                                  CPPGYALGLDNHIVTSLNSSFITDSTSSETPS---
                                                                                                                                                                                                                                                         TNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDEC
                                                                                                                                                                                                                                                                                          VCRNLPGSYGCICAAGYELLKLDGIRGYCFDIDECSQRTHGCSDQMLCENLNGSYTCL--
                                                                                                                                                                                                                                                                                                                     LCLPSPGNAQAQCTNGFD---LDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR
                                            DVDECAGLLSGGCSHECINKAGTFECGCPLGYILNDDGRSCSPALVGCPPGTQRSADGCA
                                                                                                       FACACETGFELTPDGFGCADIDECSQDYGNCSDICINLLGTHACACERGYELAKDKLSCL
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                1394
                                                                                                                                                                                                                                                                                                                                                                  22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  152269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Downes M.,
              -DINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDN
Score 558.5; 1
Pred. No. 3e-4
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dugan-Rocha S., Dunkov
                                                                                                                                                                                                                                                                                                                                                                                                                  CD29380E3162F68A CRC64;
                                                                                                                                                                                                                                                                                                                                                                     3e-47
                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                       135;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                               ----AHTCLDIDEC
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                                                                                                                                                                                                                                                                                                                                                                                    1394;
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                                                                                                                                                                                                                                       Query Match
Best Local Sim
Matches 116;
                                                                                                                                                                                                                                                                                                                        Pfam; PF01821; ANATO; 3.

Pfam; PF00808; EGF; 6.

SMART; SM00104; ANATO; 3.

SMART; SM00104; ANATO; 3.

SMART; SM00101; EGF_11ke; 5.

SMART; SM00001; EGF_11ke; 5.

PROSITE; PS01177; ANAPHYLATOXIN_1; 3.

PROSITE; PS01178; ANAPHYLATOXIN_2; 3.

PROSITE; PS01186; EGF_2; 3.
                                                                                                                                                                                                                                                                                                       PROSITE; PS01186; EGF_2; 3.
EGF-11ke domain; Glycprotein; Hydroxylation.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ162H14.1 (Fibulin 1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
Mamumalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lloyd D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; 298047; CAB62995.1; -.
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UH16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UH16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                 397
                                                        190
                                                                                  337
                                                                                                                                                                                                       16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 KGPREIQLDLEMITVNTVINFRGSSVIR-----LRIYVSQYPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387
                                                                                                                                                                                                                                                     Similarity
                        DECSF - - SEFICQHECVNQPGTYFCSCP - PGYILLDDNRSCQDINECEHRNHTCNLQQTC
                                                                           AEPCGKGHRCVNSPGSFRCECKTGYYFDGISRMCVGVNECQRYPGRLCGHKCENTLGSYL
                                                                                                    SHOCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS
                                                                                                                                                   YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCYDVDECATD 134
                                                                                                                                                                                CRP----KLQCKSGFIQD-ALGNCIGINECLSISAPCPIGHTCINTEGSYTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PADI------FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLYMTRPI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-HSIDCPTNYIHDSLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIDPIRCEEPYLRISDNR------C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNDLCMGGCINTKGSXLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGP----TVETIKVNIHTKSRTGVILAFNEAIIEISVSKYPF
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                                                                                                                                                                                                                                                                                         554 AA;
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                         59767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                   23.0%;
                                                                                                                             -----QKNVPN------CGRGYHLNEEGTRCVGVDECAPP
                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                  Score 583; DB 4;
Pred. No. 3.4e-50;
7; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                      FE285184599A2982
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                                                                                                                                                                                                                                    102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                                                                                             Length 554;
                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                    Indels
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                           455
  305
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018026
                                                                                                      Query Match
Best Local S
Matches 162
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                                                                                                                                                                                          Pfan; PF00008; EGF; 5.

SMART; SM00104; ANATO; 2.

SMART; SM00179; EGF_CA; 4.

SMART; SM00101; EGF_LIKe; 6.

SMART; SM00177; ANAPHYLATOXIN_1; UNKNOWN_1.

PROSITE; PS01117; ANAPHYLATOXIN_1; UNKNOWN_1.

PROSITE; PS011186; EGF_L; 5.

PROSITE; PS011187; EGF_CA; 8.

PROSITE; PS011187; EGF_CA; 8.

Calcium_binding; EGF-like domain; Glycoprotein; Hy.

SEQUENCE 798 AA; 87205 MW; 3BFIEE9ED54D8BF9 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 268749; CAA92962.1;
EMBL; 268219; CAA92962.1;
EMBL; 268219; CAA92483.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Lister N., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Meg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of Celegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z68749; CAA92483.1; JOINED HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lloyd C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Wilkinson J.; Submitted (JAN-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O18026; Q20903;
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
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          167
                                                                                                                                                                                                                                                                                                                                                                                                                        PF00008; EGF; 5
                                        15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLC----
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LCHDRGGEKVECSCRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRIS
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IPR000561;
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EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anaphylatoxin
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                                                                                                 50;
                                                                                              Score 577.5; DB 5;
Pred. No. 1.9e-49;
0; Mismatches 180;
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Best Local Similarity
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Pfam; PF00008; EGF; 4.

SMART; SM00104; ANATO; 2.

SMART; SM00179; EGF_CA; 5.

SMART; SM00179; EGF_LIKe; 4.

SMART; SM00179; EGF_LIKe; 4.

PROSITE; PS01178; ANAPHYLATOXIN_2; 1.

PROSITE; PS01178; ANAPHYLATOXIN_2; 1.

PROSITE; PS01186; EGF_Z; 3.

PROSITE; PS01186; EGF_Z; 3.

PROSITE; PS01187; EGF_CA; 6.

Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; SEQUENCE 681 AA; 74459 MW; 175C966305A46699 CRC64;
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042182;
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EMBL; AF013751; AAB80944.1; -.
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Acthopterygii; Neopterygii; T
Cyprinidae; Danio.
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
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                                                                                                                                                               MDECSF -- SEFLCQHECVNQPGTYFCSCP - PGYILLDDNRSCQDINECEHRNHTCNLQQT
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    MDVVS---
                                        CFNIQGGFRCLS-FDCPANYRRSGDTRPRVDRADIIRCVKSCQHNDISCVLNP--ILSHS
                                                                               CYNLOGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGCRDQPFTILYRD
                                                                                                                                                                                                                                                                                         DNSCD-GHGCINLVGSYRCECRTGFIFNSISRSCEDIDECR-NYPGRLCAHKCENILGSY
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                                                                                                                          IDECALPTGGHICSYRCHNTPGSFHCTCPASGYTLAANGRSCQDIDECLTGTHSCSESES
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  -GRSVPADIFQMQATT----
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Last sequence update)
Last annotation update)
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Pred. No. 6.3e-55;
5; Mismatches 162;
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Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity
Matches 159; Conserv
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SMART; SM00179; EGF_CA; 5.

SMART; SM00001; EGF_like; 4.

PROSITE; PS00101; ASX_HYDROXYL; 4

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01187; EGF_CA; 7.
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Q9TZS1;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Deloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99120531; PubMed-9923656; Barth J.L., Argraves K.M., Roark E.F., Little C.D., "Identification of chicken and C. elegans fibulin-1 characterization of the C. elegans fibulin-1 gene." Matrix Biol. 17:635-646(1998).
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HSSP; P16109; 1FSB.
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                                                                                                                                                                 NVPGSYSCTCNPGFTLNE------
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IPR000561;
IPR001881;
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  SEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFK
                                          ASDGRRCEDVNECTTGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGS
                                                                               --- DGRSCQDVNECATE - NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF----
                                                                                                                          NLPGTYKCKCGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQL
                                                                                                                                                                                                       ECYTGHNCGAGEECYNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCLPSPG-NAQAQCTNGFDLDRQSGQCLD-IDECRTIPEACRGDMMCVNQNGGYLCIPRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCHDRGGEKVECSCRSGFDLAPDGMACVDHIDECATLMDDCLESQRCLNTPGSFKCI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 AA; 63984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 13, [TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 596; DB 5; 27.3%; Pred. No. 1.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF_Ca.
                                                                                                                                                                                                                                                -----CQQ----LCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8EA3E8FCE0B97BE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                           -----RTLSCGTGYAMDSETERCRDVDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163;
                                                                                                                                                                                                                                                                                                                                  ----SCTDGYWLLEGQCLDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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589;

Repeat.

208;

Gaps

170 146 131 122

253 326 200 266 182 206 homologs

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Q9Y3V7
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Best Local
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InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF-Ca.
InterPro; IPR000561; EGF-Ca.
InterPro; IPR000181; EGF-Ca.
InterPro; IPR00008; EGF-Ca; 8.
SMART; SM00179; EGF-Like; 2.
SMART; SM00010; ASX_HYDROXYL; 4.
PROSITE; PS0010; ASX_HYDROXYL; 4.
PROSITE; PS01186; EGF-Ca; 9.
PROSITE; PS01187; EGF-Ca; 9.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
Hypothetical protein; Repeat.
NOW TEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TERMBLrel. 12, Created)
01-NOV-1999 (TERMBLrel. 12, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation update)
Hypothetical 63.3 kDa protein (Fragment).
DKF2F586A1519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wambutt R., Heubner D., Mewe Submitted (MAR-1999) to the EMBL; AL050095; CAB43267.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y3V7;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y3V7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
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                           432
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                               QTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV
                                                                            CTDIDECAOGAGILCTFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEA
                                                                                                        CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ
                                                                                                                                        LGSYRCSCASGFILAADGKRCEDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT
                                                                                                                                                           PGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH
                                                                                                                                                                                                                                 ECATDSHQCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANV
                                                                                                                                                                                                                                                                                                                          LCQNTKGSFYCQARQRCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC--
                      ETCHNIQGSFRCL-RFECPPNYVQVSKTKC---
                                                                                                                                                                                                   ECETGVHRCGEGQVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENT
                                                                                                                                                                                                                                                                                                                                                     LCLPSPGN----AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP
                                                                                                                                                                                                                                                                                 RTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICREGYQ-MDESNQCVDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTVGVVRQVRPIVGPFHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHTVISLPTEREFTRPEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PISATLVMTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNETCFNIQGGFRCLS-LECPENYRKSGDTVRLEKTDTIRCIKSCRPNDVNCVLDPVHTI 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYRDMDVVSGRSV--PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF----YMRQTG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   63274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      28.1%;
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                                                                                                                                                                                                                                                               -----QRNPLICARGYHASDDGTKCVDVN
                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              es H.W., Gassenhuber J., Wien EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     Score 711.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FF2F0E9B185D8AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576
                                                                                                                                                                                                                                                                                                                                                                                                      .9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                    ERTTCHDFLECQNSPARITHYQLNFQ
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   576;
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPRO0012; Asx_hydroxyl.
Interpro; IPR000561; EGF-11ke.
Interpro; IPR001881; EGF-2.
Interpro; IPR001881; EGF-Ca.
Pfam; PF00008; EGF; 6.
SMART; SM00181; EGF-CA; 9.
SMART; SM00179; EGF-CA; 9.
SMART; SM00010; EGF-11ke; 1.
PROSITE; PS001010; ASX_HYDROXYL; 3.
PROSITE; PS01186; EGF-2; 3.
PROSITE; PS01187; EGF-CA; 8.
EGF-11ke domain; Glycoprotein; Hydro SEQUENCE 495 AA; 54340 MW; C4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HBQ5;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Novel Human cDNA clones with function of growth.";
Submitted (DEC-1999) to the EMBL/GenBank/I EMBL; AF217999; AAG17241.1; -...
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu J.R., Wan D.F., Zhao X.T., Qin W.X., Huang Y., Qiu X.K., Yu J., Han L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical 54.3 kDa protéin.
Homo sapiens (Human),
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9нвQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                               413
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   364
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                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                   16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                         FNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPA
                                                         YNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPA
                                                                                                        DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC
                                                                                                                                              DIFQMQATTRYPGAYYIFQIKSGNEGRE
                                                                                                                                                                                                                                                                                                                                  CRP----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC-----
                                                                                       DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECYTGIHNCSINETC
                                                                                                                                                                                                            AEPCGKGHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL
                                                                                                                                                                                                                                 SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS
                                                                                                                                                                                                                                                                                       YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD
: || || || : :| :||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                              26.7%;
35.8%;
                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                         ---QKNVPN------CGRGYHLNEEGTRCVDVDECAPP
                                                                                                                                                                                                                                                                                                                                                                                             Score 676; DB 4;
Pred. No. 1.3e-59;
9; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zhou
Qian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydroxylation; Hy C40434E6C82E3D70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X.M.,
 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ang H.Q.,
L.P., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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H.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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Yu Y.,
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                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO1177; ANAPHYLATOXIN_1; 3.
PROSITE; PSO1178; ANAPHYLATOXIN_2; 3.
PROSITE; PSO1010; ASX_HYDBOXYL; 5.
PROSITE; PSO1186; EGF_2; 5.
PROSITE; PSO1187; EGF_CA; 9.
Calcium-binding; EGF-like domain; G1; SEQUENCE 1174 AA; 126460 MW; 8D6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O99K58, PRELIMINARY, O99K58, O1-JUN-2001 (TrEMBLrel. 1 O1-JUN-2001 (TrEMBLrel. 1 O1-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00104; ANATO; 3.
SMART; SM00181; EGF; 11.
SMART; SM00179; EGF_CA; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC005443; AAH05443.1; ... HSSP; P00736; LAPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01821; ANATO; : Pfam; PF00008; EGF; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBLN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to fibulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95488; Fbln2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
$
                                  315
                                                          982
                                                                               256
                                                                                                        923
                                                                                                                                197
                                                                                                                                                                               142
                                                                                                                                                                                                                                                     782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364
                                                                                                                                                                                                                                                                                                    al Similarity
146; Conserv
                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                            23
                  IDPIRCEEPYLRISDNRCMCPAENPGCRD------QPFTILYRDMDVVSGRSVPADIFQM
                                                                                                                                                                   QICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGF
                                                                      FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                            TLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSE
                                                                                                                                                                                                                  PYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPT
                                                                                                                                                                                                                                                                 TVNTVINFRG---SSVIRLRIYS 444
|| :: | | :| |:||
TVKMDLSRHGTVSSFVAKLFIFVS 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVFRMGPSSAVPGDSMQLAITGGNEEGFFTTRKVSPHSGVVALTKPVPEPRDL-----LL
                                                                                                      LLAADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAG
                                                                                                                                                    QLCYNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSCAAGF
                                                                                                                                                                                                                                                    ARQRCMDGF-LQDPEGNCVDINECTSLLEPCRSGFSCINTVGSYTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILCTFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPRO00020; Anaphylatoxin.
IPRO00152; Asx_hydroxyl.
IPRO00561; EGF-like.
IPRO01881; EGF_Ca.
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                               29.0%;
35.3%;
                                                                                                                                                                                                     ···················QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
17,
21,
                                                                                                                                                                                                                                                                                                  ; Score 735.5; DB 11;
; Pred. No. 3.4e-65;
61; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                 ; Glycoprotein; Hydroxylation;
8D628AC710FBA6B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              ωω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Å
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                          1174;
                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                              Repeat
                                                                                                                                                                                                                                                                                                   Gaps
                                368
                                                      1041
                                                                              314
                                                                                                      981
                                                                                                                              255
                                                                                                                                                    922
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                            Interpro; IPROJUBI; EGE_CA.

Pfam; PF01821; ANATO; 2.

Pfam; PF01821; ANATO; 2.

Pfam; PF001821; ANATO; 3.

SMART; SM00104; EGF_CA; 8.

SMART; SM001079; EGF_CA; 8.

SMART; SM001079; EGF_LIKe; 1.

PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.

PROSITE; PS01178; ANAPHYLATOXIN_2; 2.

PROSITE; PS01178; ANAPHYLATOXIN_2; 2.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS01187; EGF_LIKe domain; Glycoprotein; Hyd
SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-99120531; PubMed-9923656;

Barth J.L., Argraves K.M., Roark E.F., Li

"Identification of chicken and C. elegans
characterization of the C. elegans fibuli
Matrix Biol. 17:635-646(1998).

EMBL; AR051399; ARC05387.1;

HSSP; P00742; 1RGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               073774;
073774;
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FBLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibulin-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9031;
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                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1042
                              301
                                                                                                                                                    360
                                                                                                                            185
                                                                                                                                                                            130
                                                                                                                                                                                                    337
                                                                                                                                                                                                                                                    279
                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                           15
                  LQQTCYNLQGGFKCIDPIRCEEPYLRISDN---
                                                      SCEDIDECALPTGGHICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCS
                                                                         HCSDMDECSF -- SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCN
                                                                                                   ECSSSDQPCGEGHVCINGPGNYRCECKSGYSFDVISRTCIDINECRRYPGRLCAHKCENT
                                                                                                                                                                                                     RISP----
                                                                                                                                                                                                                           RTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICREGYQMDE-SNQCVDVD
                                                                                                                                                                                                                                                  GPAPAFAGDTISLTITKGNEEGYFVTRRLNAYTGVVSLQRSVLEPRDFALDVEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-RFDCPPNYVRVSETKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRI
                                                                                                                                                                           ECATDSHQCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRY---GYCQQLCANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QATTRYPGAYY I FOIKSGNEGREFYMROTGPISATLYMTRPIKGPREIOLDLEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
la; Aves; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000152;
IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000020; Anaphylatoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (TrEMBLrel. 07,
3 (TrEMBLrel. 07,
1 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neognathae;
                                                                                                                                                                                                                                                                                                            28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                    -----SCGRGYHLNEDGTRCVDVD
                                                                                                                                                                                                                                                                                                   ; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                  Score 722; DB 13;
Pred. No. 4.4e-64;
8; Mismatches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Eute; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .F., Little C.D.,
elegans fibulin-1
fibulin-1 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         704
                                                                                                                                                                                                                                                                                                                          DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                 Hydroxylation;
CRC64;
                 RCM--CPAENPGC-RDQPFTI
                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argraves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                           704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phasianinae;
                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                              Repeat.
                                                                                                                                                                                                                                                                                                  Gaps
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478

243

300 538 348 419

22, 70 336 129 359

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RESULT 4
Q922K8
ID Q922K8
ID Q922
AC Q922
DT 01-T
DT 0
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                                                                                                                                                        Query Match
Best Local S
Matches 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q922KB PRELIMINARY;
Q922KB;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Similar to fibulin 1.
                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC007140; AAH07140.1;
MGD; MGI:95487; Fbln1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR00020; Anaphylatoxin
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBLN1.
                                                                                                                                                      Local Similarity 36.1
nes 160; Conservative
                                                                                                                                                                                                                                                                                                                                     PF01821; ANATO; PF00008; EGF; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351
                                                    76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356
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                                                                                                                                                                                                                   PS01177; ANAPHYLATOXIN_1; UNKNOWN_3.
PS01178; ANAPHYLATOXIN_2; 3
PS0010; ASX_HYDROXYL; UNKNOWN_4.
PS01186; EGF_2; UNKNOWN_3.
PS01187; EGF_CA; UNKNOWN_B.
PS01187; EGF_CA; UNKNOWN_B.
                             YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD | | | | : : | : | | | | | | | : :
                                                                                                             CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                               CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSGRSVPADIFOMOATTRYPGAYYIFQIKSGNEGREFYMROTGPISATLVMTRPIKGPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSERMRPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTGPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYEPDDQDSCVDVDECAQALHDRRPSQDCHNLSGSYQCTCPDGYRKIGPECVDIDECRYR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYOMDESNOCYDYDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMKCINHYGGYLCLPRSAAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                     29.3%;
                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19,
19,
21,
                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                    Score 743; DB 11;
Pred. No. 3.2e-66;
5; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                           EF0D77D7F66B73B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
                                                                                                                                                    154;
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           -CGRGYHLNEEGTRCVDVDECSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                      Length
                                                                                                                                                  Indels
                                                                                                                                                                                        685;
                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus
                                                                                                                                                  Gaps
                                          134
                                                                                                                 75
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Best Local S
Matches 157
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC022497; AAH22497.1; -
SEQUENCE 683 AA; 74423 MW; 2665A3961B6403B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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TISSUE-BRAIN;
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157; Conserv
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FNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPA
                                 YNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPA
                                                                                         DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC
                                                                                                                                                               CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM
                                                                      DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGSNCQDIDECYTGIHNCSINETC
                                                                                                                                                                                                                                                                                                                                                         CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC-----
                                                                                                                                           CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI
                                                                                                                                                                                                                AEPCGKGHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL
                                                                                                                                                                                                                                      SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS
                                                                                                                                                                                                                                                                                                       YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYOM-DESNOCVDVDECATD | || : :| :||||||||
                                                                                                                                                                                                                                                                                                                                                                                             CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM-:|:| : | : | | | | : | ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ITVNTVINFRGSSVIRLRIYVS 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 737; DB 4; 1 larity 35.4%; Pred. No. 1.3e-65; Conservative 67; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
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Primates;
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21,
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Last sequence update)
Last annotation updat
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                                   363
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                      Query Match
Best Local S
Matches 226
                                                               NR MGD; MGI:1891209; Efemp2.

R MGD; MGI:1891209; Efemp2.

R InterPro; IPR000152; Asx_hydroxyl.

R InterPro; IPR000561; EGF-like.

RR InterPro; IPR001891; EGF_Ca.

InterPro; IPR001491; Thrmbomoduln.

R Pfam; PF00008; EGF; 4.

NR PRINTS; PR00907; THRMBOMODULN.

SMART; SM000179; EGF_Ca; 4.

R PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS001186; EGF_2; 4.

PROSITE; PS001186; EGF_Ca; 6.

Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;

W Matrix protein; Repeat.

SEQUENCE 443 AA; 49452 MW; 5AEC2A91048B336A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Q9JM06 PRELIMINARY; PRT; 443 AA.
Q9JM06;
Q9JM06;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20435063; PubMed=10982184;
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                    EMBL; AF109122; AAF65189.1; -.
                                                                                                                                                                                                                                                              from the multiple retinopathy critical region Hum. Genet. 106:66-72(2000).
                                                                                                                                                                                                                                                                                   Katsanis N., Venable S., Smith J.R., "Isolation of a paralog of the Doyne
                                                                                                                                                                                                                                                                                                                                                                                         EFEMP2
                       Local Sin
hes 226;
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 μ
                                  Similarity
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 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG
                       Conservative
                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                 50.78;
                    70;
                      Score 1283; D
Pred. No. 6.6e
70; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                     Lupski J.R.;
honeycomb retinal dystrophy
al region on 11q13.";
                     DB 11;
5.6e-121;
hes 135;
                      Indels
                                            Length
                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Mus
                                            443;
                      22;
                     Gaps
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R InterPro; IPR000561; EGF-11ke.
R InterPro; IPR001881; EGF_CA.
R InterPro; IPR001491; Thrmbomoduln.
R Pfam; PF00008; EGF; 3.
R Pfam; PF00008; EGF; 5.
R PRINTS; PR00907; THRMBOMODULN.
R SMART; SM00179; EGF_CA; 6.
R SMART; SM00101; EGF_L1ke; 2.
R SMART; SM00101; EGF_L1ke; 2.
R PROSITE; PS00110; ASX_HYDROXYL; 3.
R PROSITE; PS01186; EGF_CA; 5.
R PROSITE; PS01187; EGF_CA; 5.
                                                                                                                     Query Match
Best Local S
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Q9H3D5;
Q1-MAR-2001
Q1-MAR-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seibold S., Marx M.;
"Cloning of a new fibulin-like gene.";
"Cloning of Lyan-1999) to the EMBL/GenBank/DDBJ
EMBL; AF124486; AAG45245.1;
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibulin-like extracellular matrix protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 YVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYVQVSDNRCLCPASNPLCREQPSSIVHRYMSI
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                                            1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG
                                                                                                                       Similarity
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(TTEMBLrel. 16, Last sequence update)
(TTEMBLrel. 21, Last annotation update)
                                                                                             Conservative
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                                                                                                                     50.0%;
                                                                                                                     Score 1266; DB 4;
Pred. No. 3.4e-119;
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                                                                                                Mismatches 134;
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                                                                                                                                            Length 443;
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1 MPGIKRILTVTILALCLPSP.....
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Maximum Match 100%
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sp_unclassified:*
sp_rvirus:*
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sp_virus:*
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sp_archeap:*
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1 Q96TF5
Q943M6
Q943M6
1 Q92X8
Q92X8
Q97558
1 Q99K58
1 Q99K34
3 Q73774
Q948Q7
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Compugen Ltd
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Q9h3d5 homo sapien
Q922k8 mus musculu
Q8tbh8 homo sapien
Q99k58 mus musculu
Q73774 gallus gall
Q93v7 homo sapien
Q9hbq5 homo sapien
Q42182 brachydanio
                                                                    Q9tzs1 caenorhabdi
Q9uh16 homo sapien
O18026 caenorhabdi
                                              Q9vs89
                                                                                                                                                                                                                                                                                                                                                             Q96tf5 homo
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                                            6 homo sapien
6 caenorhabdi
9 drosophila
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45	44 4	43	42													29	28	27 4									18	17
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mus	homo	Q96ft5 homo sapien		Q8sss3 dictyosteli		Q14767 homo sapien	Q60789 mus musculu	ğ.	000508 homo sapien	075412 homo sapien	Q9v4b8 drosophila	Q9np01 homo sapien	ratt	mus	homo	ÖĦO	OMO	Q28019 bos taurus	Q8rlu8 mus musculu		Q9wuh9 rattus norv		mus	Q96jp8 homo sapien	Bug	Q96k89 homo sapien	Q9wuh8 rattus norv	Q96rw7 homo sapien

## ALIGNMENTS

RESULT 1
Q96TF5
ID Q96TF5
Q96TF5
AC Q96T
OT 01-T
OT 01-T
OT 01-T
OT 01-T
OT T1-T
OT T1 밁 õ Query Match Best Local Sin Matches 226; Tanaka S., Sugimachi K., Sugimachi K.;
"Human mutant p53 binding protein (MBP1).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dat
EMBL; AB030655; BAA92880.1; -.
InterPro; IPR000512; Asz\_hydroxy1.
InterPro; IPR000512; ESF-1ike.
InterPro; IPR0005181; ESF-1ike.
InterPro; IPR00181; ESF\_Ca.
Pfam; PF00008; EGF; 4.
PROSITE; PS001010; ASX\_HYDROXYL; UNKNOWN\_4.
PROSITE; PS01187; ESF\_CA; UNKNOWN\_4.
SEQUENCE 443 AA; 49421 MW; 9CE175F4F388A56D C O96TF5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mutant p53 binding protein 1 (MBP1). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; MBP1.
Homo sapiens (Human). SEQUENCE FROM N.A. Submitted (JUL-1999) Tanka SEQUENCE FROM N.A. Q96TF5 ß œ 1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG Similarity LPGSLLLWALLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSQHCRDVNECLTIPEACKG Conservative PRELIMINARY; 50.9%; Score 1289; DB 4; 49.9%; Pred. No. 1.6e-121; tive 74; Mismatches 131; to the EMBL/GenBank/DDBJ 9CE175F4F388A56D CRC64; 443 ₽ databases databases Length 443; Indels 22; Gaps 67

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                                                                                  CLPSPGNAQAQCTNGFDLDROSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
                                YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLI---
                                                               CINLPVRYTCICYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSFLCI-----
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#YDROXYLATION:
21

N-LINKED (GLCNAC...) (POTENT)
52

N-LINKED (GLCNAC...) (POTENT)
98

N-LINKED (GLCNAC...) (POTENT)
294

N-LINKED (GLCNAC...) (POTENT)
294

N-LINKED (GLCNAC...) (POTENT)
923

N-LINKED (GLCNAC...) (POTENT)
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N-LINKED (GLCNAC...) (POTENT)
1039

N-LINKED (GLCNAC...)
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N-LINKED (GLCNAC...)
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N-LINKED (GLCNAC...)
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CPAGEMASEEGTNCIDVDECLRPDVCGEGHCVNTVGAFRCEYCDSGYR 662
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CCELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY S
                                                                                                                                 52;
                                                                                                                                 Score 544; DB 1;
Pred. No. 7e-34;
2; Mismatches 134
                                                                                                                                  134;
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                         -----CRFGYQ 118
                                                                                                                                 Indels 122;
                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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	959 DVNECELLSG 968.	95	В
	343 DQPFTILYRDMDVVSG 358	34	Qy
958	899 HCVCQQGFSISADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCLCYQGFQAPQDGQGCV 95	89	Db
34:	313 KCIPAENPGCR 34:	31	Qy
898	841 DKSVCQRGDCINTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSF 891	84	Db
31:	254 SEFLCQH-ECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGF 31:	25	Q
840	781 GYQLSAAKDQCEDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCEDINECLE 84(	78	DЬ
25	220	22	Qy
780	721 CANGDESNIEGSYMESCHKGYTRTPDHKHERDIDECQQGNLCVNGQCKNTEGSERCTCGQ 780	72	Дb
219	CQQ-LCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ	177	Qy
720	663 MTQRGRCEDIDECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLEPNV 720	66	ДĎ
176	119 MDESNQCVDVDECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGY 170	11	Qy

Search completed: July 3, 2003, 18:23:14
Job time: 13.3157 secs

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RESULT 15
LTBS_HDMAN
ID LTBS_H
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AC P27064
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01-AUG-1991 (Rel. 19)
01-AUG-1991 (Rel. 19)
15-JUN-2002 (Rel. 41)
Latent transforming (Transforming growth
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19, Last sequence update)
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ITLFKVSAPNHADTEVNFELQLKTTIVGAPNVLPAIRANFL
LQKGEKRNSAVVTLRDSLDGPQTVKLQLLLRMSKGKNFNT
YAANLIUDVAAHKRHNTVHPPLMKIR -> QIADGYSCIKV
CSTEDTECLGNHTREVLYQFRAVPSLKTIISPIEVSRIVTH
MGVPFSVDYNLDYVGGRHFRIVQERNIGIVQLVKFISGPTV
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InterPro; IPR000152; Asx_hydroxy1
InterPro; IPR000561; EGF_Ca.
InterPro; IPR0002112; Fibril-assoc
pfam; PF00088; EGF; 15.
Pfam; PF000683; TB; 4.
SMART; SM00179; EGF_CA; 13.
SMART; SM00179; EGF_Like; 4.
PROSITE; PS00101; ASX_HYDROXYL; 1
PROSITE; PS00010; ASX_HYDROXYL; 1
PROSITE; PS001186; EGF_1; 2.
PROSITE; PS01187; EGF_CA; 15.
Growth factor bidding; Repeat; EGGIlycoprotein; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                  EMBL; M34057; AAA61160.1; PIR; A35626; A35626. HSSP; P00750; ITPG. GlycoSuiteDB; P22064; -... Genew; HGNC:6714; LTBP1. MIM; 150390; -...
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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EGGF-LIKE 3, CALCI
EGGF-LIKE 4, CALCI
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LATENT TRANSFORMING
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    This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          Lloyd C.R.;
Submitted (
                                                                                                                                                                                                                                                                                                                                                                       Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves "Identification of chicken and C. elegans fibulin-1 homologs characterization of the C. elegans fibulin-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                         Matrix Biol. 17:635-646(1998).
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MEDLINE-99120531; PubMed-9923656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORM; C (SHOWN HERE) AND D; ARE
PRODUCED BY ALTERNATIVE SPLICING.
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
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(See http://www.isb-sib.ch/announce/
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      Pfam; PF00008; EGF; 6.

Pfam; PF01821; ANATO; 2.

SMART; SM00104; ANATO; 2.

SMART; SM00109; EGF_CA; 6.

SMART; SM00001; EGF_like; 3.

PROSITE; PS00000; ASX_HYDROXYL; 4.

PROSITE; PS01177; ANAPYLATOXIN_1; 1

PROSITE; PS01187; EGF_CA; 8.
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758749; CAC35826.1;
7588749; CAC35827.1;
758749; CAC35827.1;
758749; CAC35817.1;
758219; CAC35817.1;
758219; CAC35818.1;
758219; CAC35818.1;
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F56H11.1b; CE26702.
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IPR000561;
IPR001881;
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      Alternative
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EGF-like.
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ANAPHYLATOXIN-LIKE I
ANAPHYLATOXIN-LIKE I
ANAPHYLATOXIN-LIKE I
EGF-LIKE 1. CALCIUM-
EGF-LIKE 2. CALCIUM-
EGF-LIKE 3. CALCIUM-
EGF-LIKE 5. CALCIUM-
EGF-LIKE 6. CALCIUM-
EGF-LIKE 7. CALCIUM-
EGF-LIKE 9. CALCIUM-
EGF-LIKE 
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(POTENTIAL).
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Matches

Extracellular matrix;

(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Genew; HGNC:3600; FBLN1.

MIN; 135820; -

InterPro; IPR000020; Anaphylatoxin.

InterPro; IPR000152; Asx_hydroxyl.

InterPro; IPR0001561; EGF-like.

InterPro; IPR0001561; EGF-like.

Pfam; PF00008; EGF; 6.

Pfam; PF00008; EGF; 7.

SMART; SM00104; ANATO; 3.

SMART; SM00104; ANATO; 3.

SMART; SM00104; EGF_LA; 7.

SMART; SM00101; EGF_L1ke; 2.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS001177; ANAPHYLATOXIN_1; 3.

PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
                                                                                                                                                                                                                                                                                                   EMBL; X53741; CAA37770.1; --
EMBL; X53742; CAA37771.1; --
EMBL; X53743; CAA37772.1; --
EMBL; U01244; AAB17099.1; --
EMBL; 29531; CAB62960.1; --
PIR; A32826; A32826
PIR; A36346; A36346.
PIR; C36346; B36346.
PIR; C36346; C36346.
PIR; C36346; C36346.
PIR; C36346; PIENN.
PIR; C36346; PIENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrict: use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 30-44.

SEQUENCE OF 30-44.

SEQUENCE OF 30-44.

MEDLINE=89354537; PubMed=2527614;

Argraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;

Fibulin, a novel protein that interacts with the fibronectin receptor beta subunit cytoplasmic domain.";

Cell 58:623-629(1989).

-I- SUBCELIULAR LCOATION: Secreted; extracellular matrix.

-I- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A, B, C AND D (SHOWN HE) PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER ONLY IN THE: TERMINAL REGIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM Argraves S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE-91100426; PubMed-2269669;
Argraves W.S., Tran H., Burgess W.H., Dickerson
"Fibulin is an extracellular matrix and plasma g
repeated domain structure.";
J. Cell Biol. 111:3155-3164(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibulin-1
FBLN1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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SIMILARITY: CONTAINS
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glycoprotein
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PROSITE; PS01187; EGF
Signal; Alternative s
Repeat; EGF-like doma
SIGNAL 1
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7; EGF_CA; 8.
tive splicing; (
e domain; Calciu
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42
77274
  27.5%;
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EFTRPEEIIFLAAITPDHPASQANIIFDITEGNLRDSFDII
KRYMDGMTVGVVFQVFFIVGPFHAVLKLEMNYVVGGVVSHR
NVVNVRLEVSSWF -> RCERLECHBNRECSKLPLRITYV
HLSFPINIQAPAVVFRMGPSSAVFGDSMQLAITGGNEEGFF
TTRKVSPHSGVVALTKPVPEPRDLLLTVKMDLSRHGTVSSF
VAKLFIFVSAEL (IN ISOFORM C).
C -> S (IN REF. 4).
HR -> SH (IN REF. 4).
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ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4.
EGF-LIKE 5.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
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Pred.
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ium-binding.
695.5; DB 1
No. 1.1e-45;
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703;

CRC64; Length

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Pfam; PF00008; EGF; 6.

Pfam; PF01008; EGF; 6.

Pfam; PF01821; ANATO; 3.

SMART; SM0010; ANATO; 3.

SMART; SM0010; EGF_1ke; 2.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00122; EGF_1; FALSE_NEG.

PROSITE; PS01177; ANAPHYLATOXIN_1; 3.

PROSITE; PS01178; ANAPHYLATOXIN_2; 3.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS01187; EGF_2; 3.
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COMAIN
DOMAIN
DISULFID
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InterPro;
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EMBL; X70853; CAA50206.1;
PIR; S36441; S36441.
HSSP; P35555; 1EMN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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[1]
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IPR000152; Asx_hydroxyl.
IPR000561; EGF-11ke.
IPR001881; EGF_Ca.
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ANAPHYLATOXIN-LIKE 1
ANAPHYLATOXIN-LIKE 2
ANAPHYLATOXIN-LIKE 2
EGF-LIKE 1. CALCIUM-
EGF-LIKE 3. CALCIUM-
EGF-LIKE 5. CALCIUM-
EGF-LIKE 5. CALCIUM-
EGF-LIKE 6. CALCIUM-
EGF-LIKE 7. CALCIUM-
EGF-LIKE 8. CALCIUM-
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ium-binding.
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CALCIUM-BINDING
E 2, CALCIUM-BINDING
E 3, CALCIUM-BINDING
E 4, CALCIUM-BINDING
E 5, CALCIUM-BINDING
E 6, CALCIUM-BINDING
E 7, CALCIUM-BINDING
E 8, CALCIUM-BINDING
E 9, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix;
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RESULT 13
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Best Local S
Matches 162
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                                                                  QVRPIVGPFYAVLKLEMNYVLGGVVSHR--NVVNVHIFVSEYWF
                                                                                                                                                                                                                                                                                                                             MTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                                                               SLPTFREFTRPEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGVVR
                                                                                                                                                    FNIQGSFRCLS-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVI
                                                                                                                                                                                                                                 YNLQGGFKCIDPIRCEEPYLRISDN-----
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 703.5; I
Pred. No. 2.7e
67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QKNVPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
.7e-46;
                                                                                                                                                                                                                     RCM--CPAENPGC-RDQPFTILYRDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156;
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663

603 353 544 305 484 248 425 189 365 134 336 75 22;

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THE PROPERTY OF THE PROPERTY O
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SIGNAL 1
CHAIN 28
DOMAIN 28
DOMAIN 178
DOMAIN 448
DOMAIN 488
DOMAIN 604
DOMAIN 679
DOMAIN 764
DOMAIN 764
DOMAIN 764
DOMAIN 901
DOMAIN 903
DOMAIN 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX. COMPONENT OF BASEMENT MEMBRANES AND OTHER CONNECTIVE TISSUES.

TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND OVAI SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X82494; CAA57876.1;
P00736; LAPQ.
                                                                 Repeat.
1184
1444
147
4444
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                                                       SUBDOMAIN NA (CYS-RICH)
SUBDOMAIN NB (CYS-FREE)
ANAPHYLATOXIN-LIKE 1
ANAPHYLATOXIN-LIKE 2
ANAPHYLATOXIN-LIKE 3
ANAPHYLATOXIN-LIKE 3
ANAPHYLATOXIN-LIKE 3
ANAPHYLATOXIN-LIKE 3
ANAPHYLATOXIN-LIKE 3
ANAPHYLATOXIN-LIKE 3
BEGF-LIKE 1, CALCIUM-BINDING
EGF-LIKE 5, CALCIUM-BINDING
EGF-LIKE 5, CALCIUM-BINDING
EGF-LIKE 6, CALCIUM-BINDING
EGF-LIKE 7, CALCIUM-BINDING
EGF-LIKE 9, CALCIUM-BINDING
EGF-LIKE 9, CALCIUM-BINDING
EGF-LIKE 10, CALCIUM-BINDING
EGF-LIKE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasma; EGF-like domain;
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                                                                                                                                                  sequence update) annotation updat
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Pred. No. 1.6e
61; Mismatches
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                                                Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                     705
                                                                                                                                                    update)
                                                                                                                             protein
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nes 156;
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                                                Muridae;
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Indels Length 1184; CRC64;

63;

Gaps

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920 184 860 129 836 70

1094

(POTENTIAL) (POTENTIAL)

(BM-90)

Euteleostomi;

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InterPro: IPRO00020; Anaphylatoxin.
InterPro: IPRO00152; Asx_bydroxyl.
InterPro: IPRO00561; EGF-11ke.
InterPro: IPRO00561; EGF-2
InterPro: IPRO01881; EGF_Ca.
Pfam; PF01821; ANATO; 2.
SMART; SM00104; ANATO; 3.
SMART; SM00104; ANATO; 3.
SMART; SM001079; EGF_CA; 9.
SMART; SM001010; ASX_HYDROXYL; 5.
PROSITE; PS001177; ANAPHYLATOXIN_1; 3.
PROSITE; PS001178; ANAPHYLATOXIN_2; 3.
PROSITE; PS001187; EGF_1; FALSE_NEG.
PROSITE; PS01187; EGF_2; 5.
PROSITE; PS01187; EGF_2; 5.
        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
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SUBDOMAIN NA (CYS-RICH).

SUBDOMAIN NA (CYS-REE).

ANAPHYLATOXIN-LIKE 1.

ANAPHYLATOXIN-LIKE 2.

ANAPHYLATOXIN-LIKE 2.

ANAPHYLATOXIN-LIKE 3.

ANAPHYLATOXIN-LIKE 3.

EGF-LIKE 1.

ANAPHYLATOXIN-LIKE 3.

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

CALCIUM-BIND
EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 5.

CALCIUM-BIND
EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BIND
EGF-LIKE 9.

CALCIUM-BIND
EGF-LIKE 10.

EGF-LIKE 10.

CALCIUM-BIND
EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 1
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CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
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                             SEQUENCE FROM N.A.
TISSUE-Fibroblast;
MEDLINE-95104855; PubMed-7806230;
Zhang R.-Z., Pan T.-C., Zhang Z.-
Chu M.-L.;
"Fibulin-2 (FBLN2): human cDNA se
of the gene on human and mouse ch
Genomics 22:425-430(1994).
-1- FUNCTION: ITS BINDING TO FIBH
     FUNCTION: ITS BINDING CALCIUM DEPENDENT. SUBUNIT: HOMOTRIMER; I
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Query Match
Best Local S
Matches 146
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46; Conservative
GPAPAFAGDTISLTITKGNEEGYFVTRRLNAYTGVVSLQRSVLEPRDFALDVEM
                                                                                                                           FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                                                                   QICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGF
                                                                      IDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQM
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                           QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM
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BY SIMILARITY.

BY SIMILARITY.

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MISSING (IN ISOFORM 2).

HSGRKYAAGHTVHLSSCRAC -> TVAVS

GF (IN REF. 2).

G -> L (IN REF. 2).

Q -> E (IN REF. 2).

Q -> E (IN REF. 2).
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Pred. No. 2.5e-4
50; Mismatches
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.2\_HUMAN STANDARE FBL2\_HUMAN STANDARE P98095; 01-NOV-1995 (Rel. 32, C 01-NOV-1995 (Rel. 32, L 16-OCT-2001 (Rel. 40, L Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=9606; Homo sapiens FBLN2 Fibulin-2 precursor. (Human). etazoa; Chordata; theria; Primates; STANDARD; Created)
Last sequence update)
Last annotation update) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. PRT; 1184 ₽

PubMed=7806230; T.-C., Zhang Z.-Y.,

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SOME OTHER LIGANDS

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                                                                                   FNETCFNIQGGFRCLS-LECPENYRKSGDTRCERLPCNENKECQSLPLRITYYHLSFPTN
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EGF-LIKE 7, CALCIUM-BINDIN
EGF-LIKE 8, CALCIUM-BINDIN
EGF-LIKE 9, CALCIUM-BINDIN
EGF-LIKE 9, CALCIUM-BINDIN
BY SIMILARITY.
BY SIM
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Pred. No. 5.3e
56; Mismatches
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E 7, CALCIUM-BINDING
E 8, CALCIUM-BINDING
E 9, CALCIUM-BINDING
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Mammalia; Eutheria;
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entities requires a license
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Eur. J. Biochem. 263:471-477(1999).
-i- FUNCTION: ITS BINDING TO FIBRONECTIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Fibroblast;

MEDLINE-94064787; PubMed-8245130;

Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu
"Structure and expression of fibulin-2, a novel extracellular
protein with multiple EGF-like repeats and consensus motifs fo
calcium binding.";
Cell Biol. 123:1269-1277(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Extracellular matrix.
ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown 2/EGF3-less; are produced by alternative splicing. TISSUE SPECIFICITY: COMPONENT OF BOTH BASEMENT MEMBER CONNECTIVE TISSUES.
SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
; X75285; CAA53040.1;
AF135253; AAD34456.1;
AF135239; AAD34456.1;
AF135240; AAD34456.1;
AF135241; AAD34456.1;
AF135242; AAD34456.1;
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AF135249; AAD34456.1;
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AF135251; AAD34456.1;
AF135252; AAD34456.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALCIUM DEPENDENT.
SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED SUBCELLULAR LOCATION: Extracellular magnetic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIOMOLTRHGTVNTFI----
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Sciurognathi; Muridae;
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EGF-like domain; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation;
                                                CIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTR
                                                                                                                                          PGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF
                                                                                                                                                                                                                 RILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV
                                                                                                                                                                                           THNCRADQVCINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCS
                                                                                                                                                                                                                                                                 AAVAGPEMOTGRNNFVIRRNPADPORIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAG
                                                                                                                                                                                                                                                                                                                                       NHYGGYLCLPKTAQIIVNNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASA
                                                                                                                                                                                                                                                                                                                                                                       NONGGYLCIPRTNPVY---RGPYSNPY-------
                                                                                                                                                                                                                                                                                                                                                                                                            KALFLIMLTLALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDACKGGMKCV
                                                                                                                        PGFQLAANNYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493
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i) EGF_1ike; 2.
ii) ASX_HYDROXYL; 4.
ii) EGF_1; FALSE_NEG.
ii) EGF_2; 4.
iii) EGF_CA: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
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MATRIX PROTEIN 1

EGF-LIKE 1, DIVERGENT.

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 5, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()

EGF-LIKE 5, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()

EG
                                                                                                                                                                                                                                                                                     ---APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1101; Dr
Pred. No. 1.2e-
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R -> W (IN MVLT).
/FTId=VAR_009513.
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les 162;
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# 2).

# 3).

# 4).
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(POTENTIAL).
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 Calcium-binding.
SIGNAL 1
CHAIN 26
DOMAIN 33
DOMAIN 110
DOMAIN 117
DOMAIN 177
DOMAIN 217
DOMAIN 263
DOMAIN 309
DOMAIN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBL1_CHICK
073775;
16-0CT-2001
16-0CT-2001
15-JUN-2002
                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianidae; Phasiani
                                                                                                                                              PROSITE;
                                                                                                                                                                                                                   Pfam; PF00008; EGF; 6.
Pfam; PF01821; ANATO; 2.
'SMART; SM00104; ANATO; 3.
SMART; SM00179; EGF_CA; 8.
SMART; SM00001; EGF_like;
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDILINE-99120531; PubMed-9923656;

MEDILINE-99120531; PubMed-9923656;

Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves the C. elegans fibulin-1 homoly characterization of chicken and C. elegans fibulin-1 gene.";

matrix Biol. 17:635-646(1998).

-i- SUBCELIULAR LOCATION: Secreted; extracellular matrix.

-i- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
                                                                                                                                   Signal;
                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibulin-1
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HSSP; P00742; 1
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                                                                                                                                   Glycoprotein;
                                                                                                                                                        PS00010; ASX_HYDROXYL; 5.
PS01177; ANAPHYLATOXIN_1;
PS01178; ANAPHYLATOXIN_2;
PS01022; EGF_1; FALSE_NEG
PS01186; EGF_2; 3.
                                                                                                                                                                                                                                                                                                     IPR000020;
IPR000152;
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IPR001881;
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(Rel. 40,
(Rel. 41,
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                                                                                                                                                                                                                                                                                                                                          AAC05388.1;
                                                                                                                                              EGF_1; 1
EGF_2; :
EGF_CA;
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EGF-like.
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                                                                                                                                   Extracellular matrix; Repeat;
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ANAPHYLATOXIN-LIKE 1
ANAPHYLATOXIN-LIKE 3
EGF-LIKE 1
EGF-LIKE 2, CALCIUM
EGF-LIKE 3, CALCIUM
EGF-LIKE 4, CALCIUM
EGF-LIKE 5, CALCIUM
                                                                                                           POTENTIAL.
                                                                                                 FIBULIN-1
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, CALCIUM-BINDING
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, CALCIUM-BINDING
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                                                              بر در س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Argraves
homologs
                                                                                                                                   EGF-like domain;
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             (POTENTIAL).
(POTENTIAL).
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SIGNAL
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PROSITE;
PROSITE;
PROSITE;
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                                                     YVSQYPF
                                                                                                                                   QIKSGNEGREFYMRQTGPISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI 441
                                                                                                                                                                                                 DPYVLTSENRCVCPVSNTMCRDVPQSIVYKYMNIRSDRSVPSDIFQIQATTIVANTINTF
                                                                                                                                                                                                                                EPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIF
                                                                                                                                                                                                                                                                                                        CVNEPGKFSCMCPGGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPQNPCQ
                                                                                                                                                                                                                                                                                                                                          CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCE
                                                                                                                                                                                                                                                                                                                                                                                                                NYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQ
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                                                                                               RIKSGNENGEFYLRQTSPVSAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLTI
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PS00022;
PS01186;
PS01187;
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EGF-LIKE 2, CALCIUM-BINDING (I
EGF-LIKE 3, CALCIUM-BINDING (I
EGF-LIKE 4, CALCIUM-BINDING (I
EGF-LIKE 5, CALCIUM-BINDING (I
EGF-LIKE 6, CALCIUM-BINDING (I
EGF-LIKE 4, CALCIUM-BINDING (I
EGF-LIKE 3, CALCIUM-BINDING (I
EGF-LIKE 4, CALCIUM-BINDING (I
EGF-LIK
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Pred.
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EGF-CONTAINING FIBULIN-LIKE
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RESULT

InterPro; InterPro;

IPR000152;
IPR000561;
IPR001881;

601548; 126600;

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EMBL; U03877; AAA65590.1; HSSP; P35555; 1EMN.
                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                              entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             Mackey D.A.,
Schorderet D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLING=3023231, Munier F.L., H
Stone E.M., Lotery A.J., Munier F.L., H
Vandenburgh K., Cousin P., Nishimura D.
Vandekev D.A., Hagerman G.S., Bird A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=97001163; PubMed=8812496;

Ikegawa S., Toda T., Okui K., Nakamura Y.

"Structure and chromosomal assignment of that is highly homologous to fibrillin.";
                                                                                                                                                                                                                                                                                                                                                                                                             "A single EFEMP1 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT DHRD/MLVT TRP-345, AND VARIANT PHE-220.
MEDLINE=99295941; PubMed=10369267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence, recombinant expression and tissue extracellular matrix proteins, fibulin-3 and Matrix Biol. 18:469-480(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20068041; Pul
Giltay R., Timpl R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=95097983; PubMed=7799918;
Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;
"An overexpressed gene transcript in senescent and quifibroblasts encoding a novel protein in the epidermal like repeat family stimulates DNA synthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 41, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein 1 precursor (Fibulin-3) (Fibrillin-like protein) (Extracellular protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Skin;
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                                                                                                                                                                                                                                                                       Doyne honeycomb retinal dystrophy.";

Genet. 22:199-202(1999).

SUBCELLULAR LOCATION: Secreted.

ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4;

be produced by alternative splicing.

DISEASE: DEFECTS IN EFEMPL ARE A CAUSE OF DOYNE HONEYCOMB RET
DYSTROPHY (DHRD) ALSO KNOWN AS MALATTIA LEVENTINESE (MLYT OR
AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY YELLOW-WHITE
DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                   PIGMENT EPITHELIUM.
                                                                        HGNC:3218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35:590-592(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                Hagerman G.S., F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                          EFEMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10601734;
R., Kostka G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                            associated with both malattia ldystrophy.";
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Heon E., Piguet B.
D., Swiderski R.E.,
, Sheffield V.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493
                                                                                                                                                                        There are no restrictions ong as its content is in
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Silvestri
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DOMAIN
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SIGNAL
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SMART; SM00179; EGF_CA; 4.
SMART; SM00001; EGF_11ke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 18:3608-3616(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            properties."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallagher W.M., Argentini Conseiller E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99308589; PubMed-10380882; Gallagher W.M., Argentini M., Sier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "MBP1: a novel mutant p53-specific protein partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                         Local Similarity
les 226; Conser
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SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS
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PS00022;
MPGIKRILTYTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
IPR001491; Thrmbomoduln.
                                                                                         198
394
443
                                         Conservative
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207
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25
443
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EGF_2; 4.
EGF_CA; 6.
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ASX_HYDROXYL;
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                                                   50.6%;
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                                                                                     EGF-LIKE 1, DIVERGENT.
EGF-LIKE 2, CALCIUM-BINDING (POTENTILE EGF-LIKE 3, CALCIUM-BINDING (POTENTILE EGF-LIKE 4, CALCIUM-BINDING (POTENTILE EGF-LIKE 5, CALCIUM-BINDING (POTENTILE EGF-LIKE 5, CALCIUM-BINDING (POTENTILE EGF-LIKE 6, CALCIUM-BINDING (POTENTILE) EFF SIMILARITY.

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Pred. No. 1.9e
70; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sierra V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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                                        DB 1;
1.9e-90;
nes 135;
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                                                               Length 443;
                                        Indels
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035568;
16-0CT-2001
16-0CT-2001
16-0CT-2001
                                                                                                                    entities
or send a
             InterPro; IPR00
Pfam; PF00008;
SMART; SM00179;
                                                                                                                                                                                                                                                                                              Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung
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 SM00001;
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  ; EGF; 3.
9; EGF_CA; 4.
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                 "Interaction of DA41, a DAN-binding protein, with factor-like protein, S(1-5)."; Biochem. Biophys. Res. Commun. 237:245-250(1997).-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein 1
(Fibulin-3) (FIBL-3) (T16 protein).
                   EMBL; D89730; BAA22265.1; -. HSSP; P3555; 1EMN.
InterPro; IPR000152; Asx_hyd
InterPro; IPR000561; EGF-lik
                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97415782; Poor Ozaki T., Kondo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFEMP1 OR FBLN3.
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                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
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  IPR001881;
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                     Asx_hydroxyl.
EGF-like.
EGF_Ca
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EGF\_like;

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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001491; Thrmbomoduln.
Pfam; PF00008; EGF; 4.
PRINTS; PR00907; THRMBOMODULN.
SMARY; SM00179; EGF_CA; 4.
SMARY; SM00101; EGF_11ke; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01186; EGF_CA; 6.
PROSITE; PS01187; EGF_CA; 6.
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EMBL; AF093119; AAC62108.1;
EMBL; AF109121; AAF65188.1;
EMBL; BC010456; AAH10456.1;
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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TISSUE-Melanoma;
MEDLINE-20068041; PubMed-10601734;
MEDLINE-20068041; PubMed-10601734;
                                                                                                                             CHAIN
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Submitted /
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MEDLINE=20435063; PubMed=10982184;

MEDLINE=20435063; PubMed=10982184;

Katsanis N., Venable S., Smith J.R., Lupski J.R.;

Katsanis N., Venable S., Smith J.R., Lupski J.R.;

"Isolation of a paralog of the Doyne honeycomb retinal from the multiple retinopathy critical region on 11q13.

Hum. Genet. 106:66-72(2000).
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"Sequence, recombinant expression
extracellular matrix proteins, fil
Matrix Biol. 18:469-480(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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EGF-containing fibulin-like extracellular matrix protein
(Fibulin-4) (FIBL-4) (UPH1 protein).
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604633; -.
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Primates;
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POTENTIAL.

EGF-CONTAINING FIBULIN-LIKE EX BGF-CONTAINING FIBULIN-LIKE EX MATRIX PROTEIN 2.

EGF-LIKE 1, DIVERGENT.

EGF-LIKE 3, CALCIUM-BINDING (P EGF-LIKE 3, CALCIUM-BINDING (P EGF-LIKE 4, CALCIUM-BINDING (P EGF-LIKE 5, CALCIUM-BINDING (P EGF-LIK
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Matches 226
                                      FBL4_MOUSE STANDARD; PRT; 443 AA. 09WVJ9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) EGF-containing fibulin-like extracellular matrix (Fibulin-4) (FIBL-4) (Mutant p53 binding protein
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Mus musculus (Mouse)
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Similarity
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YVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF
                       IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                                  NHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPETILYRDMDV
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Pred. No. 5.7e-91;
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MBP1.

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

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_FBL4_CRIGR STANDARD; PRT; 443 AA.
O55058;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein
(Fibulin-4) (FIBL-4) (H411 protein).
EFFEMP2 OR FBLN4.
                                                                    EMBL; AF046870; AAC03101.1;
HSSP; P00736; 1AP0.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                          use by non-profit institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                Heine H., Delude R.L., Monks B., Golenbock D.T. Submitted (FEB-1998) to the EMBL/GenBank/DDBJ-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
SMART; SM00179; EGF_CA; 4.

SMART; SM00001; EGF_11ke; 2.

PROSITE; PS00010; ASX_HYDROXYL;

PROSITE; PS00022; EGF_1; FALSE_N

PROSITE; PS01186; EGF_2; 4.
                                                                                                                                                                                                                                                                                                                                                             Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                               InterPro; IPRO
Pfam; PF00008;
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                                                                                                                                                                                                                                                                                                    TISSUE-Ovary;
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                                                               EGF;
            FALSE_NEG
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Matches 227; Conserv
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                       IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF
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                                                                                                            VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1290; DB 1;
Pred. No. 4.8e-91;
71; Mismatches 133;
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E 2, CALCIUM-BINDING
E 3, CALCIUM-BINDING
E 4, CALCIUM-BINDING
E 5, CALCIUM-BINDING
E 6, CALCIUM-BINDING
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FBL4\_HUMAN STAN 095967; 075967; 16-OCT-2001 (Rel. 4 16-OCT-2001 (Rel. 4

40, Creat 40, Läst

sequence

Created)

STANDARD;

PRT;

443 Ą

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Best Local S
Matches 422
J.5_MOUSE

PRT; 448 AA.

PRT; 448 AA.

O9WVH9;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

E Fibulin-5 precursor (FIBL-5) (Developmental arte

E EGF-like protein) (Dance).

E EGF-like protein) (Dance).

S Mus musculus (Mouse).

S Eukaryota; Metazoa; Chordata; Craniata; Vertebra

C Eukaryota; Butheria; Rodentia; Sciurognathi; Muri
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EGF-LIKE 6, CALCIUM-BII
CELL ATTACHMENT SITE (
BY SIMILARITY
B
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Pred. No. 7.8e
11; Mismatches
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-- LNKED (GLCNAC. . .) (POTENTIAL).
-- P (IN REF. 2).
-- E6BC68F7BF14B714 CRC64;
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      Vertebrata; |
thi; Muridae;
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7.8e-176;
nes 15;
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HSSP; P00736; 1APQ.
MGD; MGI:1346091; Fb1n5.
InterPro; IPR000152; Asx_hydroxyl
InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF-Ca.
Pfam; PF00008; EGF; 4.
SMART; SM00179; EGF_CA; 4.
SMART; SM00179; EGF_Like; 2.
PROSITE; PS00022; EGF_1; FALSE_NE
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 6.
PROSITE; PS01187; EGF_CA; 6.
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"DANCE, a novel secreted RGD protein expressed in developing, atherosclerotic, and balloon injured arteries.";

J. Biol. Chem. 274:22476-22483(1999).

1- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR DEVELOPMENT AND REMODELING.

1- SUBCELLULAR LOCATION: Secreted.

1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

This SWISS-DOOT
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Nakamura T., Ruiz-Lozano P., Lindner V., Yabe
Furukawa Y., Kobuke K., Tashiro K., Lu Z., Ar
Matsumori A., Sasayama S., Chien K.R., Honjo
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EGF-LIKE 1, DIVERGEE
EGF-LIKE 2, CALCIUM
EGF-LIKE 3, CALCIUM
EGF-LIKE 4, CALCIUM
EGF-LIKE 5, CALCIUM
EGF-LIKE 6, CALCIUM
EGF-LIKE 6, CALCIUM
EGF-LIKE 7, CALCIUM
EGF-LIKE 6, CALCIUM
EGF-LIKE 6, CALCIUM
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Score 2405; Description of the 
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E 3, CALCIUM-BINDING
E 4, CALCIUM-BINDING
E 5, CALCIUM-BINDING
E 6, CALCIUM-BINDING
E 6, CALCIUM-BINDING
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HGNC:3602; FBLN5

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SMART; SM00001; EGF_like; 2.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00022; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_2; 4.

PROSITE; PS01187; EGF_CA; 6.
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IPR000561;
IPR001881;
VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL
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E 2, CALCIUM-BINDING
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InterPro: IPRO00561; EGF-like.
InterPro: IPRO00501881; EGF_Ca.
InterPro: IPRO01881; EGF_CA:
Pfam; PF00008; EGF; 4.
SMART; SM000017; EGF_LIKe; 2.
SMART; SM00001; EGF_LIKe; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4
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KOWAI R.C., Richardson J.A., Miano J.M., Olson E.N.;
"EVEC, a novel epidermal growth factor-like repeat-containing prote:
upregulated in embryonic and diseased adult vasculature.";
Circ: Res. 84:1166-1176(1999).
-1- FUNCTION: PROMOTES ADDESION OF ENDOTHELIAL CELLS THROUGH
INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
                                                                         SIGNAL
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (EVEC).
Fiblio OR DANCE.
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EMBL; AF137350; AAD25101.1;
HSSP; P00736; IAPQ.
                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99357779; PubMed=
Nakamura T., Ruiz-Lozano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                          between
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                                                                                                     PROSITE;
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DEVELOPMENT AND REMODELING.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAT
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61; EGF-like.
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EGF_2; 4
EGF_CA; 6.
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-Lozano P., Lindner V.,
                                                                                                                                                                                                                                                                                                                  license agreement
                                                                                      Calcium-binding; Glycoprotein;
FIBULIN-5.
EGG-LIKE 1, DIVERGENT.
EGG-LIKE 2, CALCIUM-BINDING
EGG-LIKE 3, CALCIUM-BINDING
EGGF-LIKE 4, CALCIUM-BINDING
                                                                          POTENTIAL.
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Z., Andon N.L.,
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ALIGNMENTS	NOTC_XENLA NTC3_HUMAN	CD93_MOUSE	NTC1_BRARE CD93_HUMAN	NEL2_RAT NOTC_DROME	NEL_CHICK NTC4_MOUSE	NEL1_RAT
			P46530 brachydanio Q9npy3 homo sapien			

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COLON BUT ALSO IN KIDNEY, PARCREAS, TESTIS, LUNG, AND PLACENTA.  NOT DETECTABLE IN BRAIN, LIVER, THYMUS, PROSTATE, OR PERIPHERAL  1. SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  1. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; AJ133490; CAB38568.1; - EMBL; AF112152; AAD41768.1; - EMBL; AF903118; AAC62107.1; - EMBL; AF90318; AAC62107.1; - EMBL; AF90318; AAC62107.1; -	UENCE FROM N.A.  SUB-Urine;  GLR., Sholto O., Shaul Y.; mitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  MICCION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROU INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN V DEVELOPMENT AND REMODELING.  SUBCELLULAR LOCATION: SECRETED.  TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART, TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART,	SEQUENCE FROM N.A.  TISSUE=Melanoma;  ROStka G.;  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  [2]  SEQUENCE FROM N.A.  MEDLINE=99357779; PubMed=10428823;  MEDLINE=99357779; PubMed=10428823;  Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,  Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  Matsumori A., Sasayama S., Chien K.R., Honjo T.;  "DANCE, a novel secreted RGD protein expressed in developing,  atherosclerotic, and balloon-injured arteries.";  J. Biol. Chem. 274:22476-22483(1999):	RESULT 1  FBL5_HUMAN  FBL5_HUMAN  GYBMS; O75966;  AC Q9UBS; O75966;  DT 16-CCT-2001 (Rel. 40, Created)  DT 16-CCT-2001 (Rel. 40, Last sequence update)  DT 16-CCT-2001 (Rel. 40, Last annotation update)  DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest  DE EGF-like protein) (Dance) (Urine p50 protein) (UP50).  GN FBLMS OR DANCE.  OS Homo saplens (Human).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TaxID=9606;  RN [1]

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fibrillin I - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C;Accession: A55567
R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
Genomics 23, 480-485, 1994
C*Title: Sequence of the coding region of the bovine fibrillin cDNA and localization Reference number: A55567; MUID:95137597; PMID:7835900
T;Accession: A55567; MUID:95137597; PMID:7835900
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A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-2871 <TIL>
A:Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428
C:Superfamily: fibrillin 1; EGF homology
F:1201-1236/Domain: EGF homology <EGF>
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fibrillin 1 precursor - human (fragment)
(;Specles: Homo sapiens (man)
(;Specles: Homo sapiens (man)
(;Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
(;Accession: A47221; I54355; SI7064; I59574; SI7062; S62111; A34198
R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993
A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain A;Reference number: A47221; MUID:94010947; PMID:7691719
A;Accession: A47221
A; Molecule type: mRNA
A; Residues: 1-337, 'T', 339-1029 < COR>
A; Cross references: GB: X63556
A; Cross references: GB: X63556
R; Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; S
Hum. Mol. Genet: 2, 961-968, 1993
A; Tille: Genomic organization of the sequence coding for
A; Reference number: 154355; MUID: 93372860; PMID: 8364578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOPFTILYRDMDVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYQLSAAKDQCEDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCEDINECLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDESNQCVDVDECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGY 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCVCQQGFSISADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCLCYQGFQAPQDGQGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEFLCOH-ECVNOPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANGDCSNLEGSYMCSCHKGYTRTPDHKHCRDIDECQQGNLCVNGQCKNTEGSFRCTCGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTQRGRCEDIDECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLEPNV
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llarity 29.4%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                    -VNECELLSG
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Pred. No. 3.5e-28;
2; Mismatches 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134;
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                       fibrillin,
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                                                             Pangilinan,
                       the defective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1030-3002 <MAS>
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                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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A; Cross-references: EMBL: X63556
R; Dietz, H.C.; Valle, D.; Francomano, C.A.; )
Science 259, 680-683, 1993
A; Title: The skipping of constitutive exons:
A; Reference number: I59574; MUID: 93157831; Pi
A; Accession: I59574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: fibrillin 1; EGF homology
C;Superfamily: fibrillin 1; EGF homology
C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein E;1-3002/Product: fibrillin (5' region exon A splice form) (fragment) *status predict F;132-3002/Product: fibrillin (5' region exon C splice form) *status predicted <MATC> F;132-307/Domain: EGF homology <EGF2>
F;1457-1492/Domain: EGF homology <EGF2>
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A; Residues: 1166-1176, 'X',1178-1180, 'D',1182-1185 < LEE2>
R; Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
J. Title: Connective tissue microfibrils. Isolation and characterization
A; Title: Connective tissue microfibrils. Isolation and Characterization
A; Reference number: A34198; MUID:90078246; PMID:2512293
A; Accession: A34198
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A; Residues: 565-575;1890-1892,'I',1894-1900 <
C; Comment: Fibrillin is a major component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Nature 352, 334-337, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; A;Accession: S62111
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A; Residues: 'VLVTVVFIFLSYNKML', 944-1444 <LEE1>
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A; Residues: 2217-2288, 'I', 2290-2325 <RES>
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A;Molecule type: mRNA
A;Residues; 132-3002 <PER>
A;Cross-references: GB:L13923; NID:g306745; PIDN:AA
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SIMNGGCETFCTNSEGSYECSCQPGFALMPDQRSCTDIDEC-EDNPNICDGGQCTNIPGE
                                                                                          RY--GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP-
                                                                                                                                                                                                                                                                                     GYOMDES-NOCYDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRNTIGSFKCRCDSGFALDSEERNCTDIDECRISPDLC-GRGQCVNTPGDFEC--KCDEG
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homology <EGF1>
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Pred. No. 3.9e-27;
0; Mismatches 125
                                                                                                                                                                                                                                                                                                                                                                                          -MMMKNCMDIDECQRDPLLCRGGVCHNTEGSYRCECPP
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Sakai, L.Y.
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C; Species: Ca
C; Date: 15-Oc
C; Accession:
R; Wilkinson,
submitted to
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C.Species: Caenorhabditis elegans
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C.Accession: T43210
R.Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S. submitted to the EMBL Data Library, June 1998
A.Description: Identification of chicken and C. elegans fibulin-1 homologs & A.Reference number: 222337
A.Accession: T43210
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-589 <BAR>
A.Cross-references: EMBL:AF070477; PIDN:AAC24035.1
C.Genetics:
                                   hypothetical protein F56H11.1 - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T22793; T24489
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                                                                                                                  RESULT 12
T22793
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C; Species: Caenorhabditis elegans
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Matches 159;
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J.
the EMBL Data
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                                                                                                                                                                                       SGP----TVETIKVNIHTKSRTGVILAFNEAIIEISVSKYPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCHDRGGEKVECSCRSGFDLAPDGMACVDHIDECATLMDDCLESQRCLNTPGSFKCI---
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Pred. No. 6.3e-32;
 January
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A; Reference number: Z19897
A; Accession: T24489
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-798 (WII)
A; Residues: 1-798 (WII)
A; Cross-references: EMBL: Z68219; PIDN: CAA92483.1; GS
A; Experimental source: clone T05A1
C; Genetics:
C; Genetics: EX5H11.1
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A; Accession: T22793
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-798 <WILD
A; CTOSS-references: EMBL:Z68749; PIDN:CAA92962.1; G;
A; Experimental source: Clone F56H11
R; Lloyd, C.
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A; Introns: 14/1; 92/3; 14
C; Superfamily: fibulin-1;
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                                                                                                                                                    APNHADTEVNFELQLKTTIVGAPNVLPAIRAN----FLLQKGEKRNSAVVTLRDSLDGP
                                                                                                                                                                                                                                                                                                      KGSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNE
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                                                                                                                                                                                       ----ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLYMTRPIKGP
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26.7%; Pred. No. 1.46
Live 50; Mismatches
                                                                                                                                                                                                                                                                 -CMCPAENPGCRDQPFTILYRDMDVVSGRSVP---
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C; Superfamily:
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A;Cross-references: EMBL:AF051401; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, submitted to the EMBL Data Library, February 1998
A;Description: Isolation of chicken and nematode fibulin-1 homologs A;Reference number: Z22267
A;Accession: T42760
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                                                                           EFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                                       -DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS
                            SDGRRCEDVNECTTGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSG
                                                                                                                                                                               LPGTYKCKCGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLA
                                                                                                                                                                                                                                                                                                                                                                                             PVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECSF - - SEFLCQHECVNQPGTYFCSCP - PGYILLDDNRSCQDINECEHRNHTCNLQQTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
                                                           INTKGSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%; Score 606.5;
27.3%; Pred. No. 1.50
Live 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-related proteins; EGF homology
                                                                                                                                                                                                                                                                         ------CQQ----LCA-----
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ches 163;
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T42990
fibulin 1, splice for C: Species: Caenorhabc C: Date: 11-Jan-2000 # C: Accession: T42990
R: Barth, J.L.; Argrav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: FBLN1
C; Superfamily:
C; Keywords: al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little submitted to the EMBL Data Library, February 1998 A;Description: Isolation of chicken and nematode 1 A;Reference number: Z22267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z22267
A;Accession: T42990
A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-712 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ibulin 1, splice form C precursor - Caenorhabditis
;Species: Caenorhabditis elegans
;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TDSHQCNPTQICINTEGGYTC------SCTDGYWLLEGQCLDIDE
VVTLRDSLDGPQTVKLQL
                            TLVMTRPIKGPREIQLDL 420
                                                                                                                                                                                                  EFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                                                                                                                                                           -DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF----S
                                                                                                                                                                                                                                                                                                       LPGTYKCKCGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLA
                                                                                                                                                                                                                                                                                                                                                                                                                           LGSHDCGPLYQCRNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDE
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                                                                                                                     -HSIDCPTNYIHDSLNKNRCNRQPSACGLPEE--
                                                                                                                                                                                                                                           SDGRRCEDVNECTTGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSG
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                                                           HRPAITLFKVSAPNHADTEVNFELQLKTTIVGAPNVLPAIRAN--
                                                                                                                                                   IDPIRCEEPYLRISDNR------CMCPAENPGCRDQPFTILYRDMDVVSGRSVP---
                                                                                                                                                                                 NDLCMGGCINTKGSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC
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                                                                                       ----ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 599.5; DB 2
Pred. No. 4.4e-32;
7; Mismatches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      basement membrane;
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                                                                                                                     -CSKVPLFLTYQFISL--ARAVPISS
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                                                           -FLLQKGEKRNSA
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N;Alternate names: basement membrane protein BM-90; calcium-binding protein BM-90 C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S34968; S36441; S13814
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
R;Pan, T.D.; Filler Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent Reference number: S34968; MUID:93358897; PMID:8354280
R;Reference number: S34968; MUID:93358897; PMID:8354280
R;Rean, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
R;Reference number: S36481
R;Residues: 1-705 CPANP
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
R;Residues: 1-705 CPANP
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
R;Residues: 1-705 CPANP
R;Rein, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
R;Residues: 1-705 CPANP
R;Ruge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur, J. Biochem: 193, 651-659; 1990
R;Ritle: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared
R;Residues: 28-31-49/x, 51-53; XX/,110-117;231-240, X.,242-243;339-362, S.,364-387;434-
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrification of status predicted cMATP
F;12-9/Comatn: signal sequence status predicted cMATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTDIDECAQGAGILCTFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse
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                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:278285; OMIM:1
A;Map position: 22q13.3-22q13.3
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing
C;Keywords: alternative splicing
F;180-214/Domain: EGF homology <EGFT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
B36346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibulin 1 precursor, splice form B - human
C;Species: Homo sapiens (man)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
                                            Qy
                                                                                             В
                                                                                                                                   ρ
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A; Residues: 1-601 <ARG>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated A;Reference number: A36346; MUID:91100426; PMID:2269669 A;Accession: B36346
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           В
                                                                                                                                                                                                                                                                      F;485-523/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: FBLN1; FBLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Cell Biol.
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                                                                                                                                                                                    Matches
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                                                                                                                                                                                    121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
                                                                                                                                                                                                      Similarity
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                                                                                               CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVRPIVGPFYAVLKLEMNYVLGGVVSHR--NVVNVHIFVSEYWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF
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                                                 YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
                                                                                                                                       CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNIQGSFRCLS-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI
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                                                                                                                                                                                  Conservative .
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:X53742; NID:g31416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H.; Burgess, W.H.;
                                                                                                                                                                                                    24.48;
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                                                                                                                                                                                                                                                                                                                                                                           OMIM:135820
                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                                 Score 619; DB 2;
Pred. No. 2e-33;
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                                                                                                                                                                                    97;
             -CGRGYHLNEEGTRCVDVDECAPP
                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PID: 931417
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A;Title: Fibulin, a r
A;Reference number: A
A;Reference number: A
A;Accession: A32826
A;Molecule type: prot
A;Residues: 30-35,'S)
      A;Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R. Eur. J. Biochem. 240, 427-434, 1996
A;Title: Different susceptibilities of fibulin-1 and fibulin-A;Reference number: S74094; MUID:96439073; PMID:8841408
                                                                                                                                     A49457

fibulin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text
C:Accession: A49457; S74095
R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timp
J. Cell Biol. 123, 1269-1277, 1993
A:Title: Structure and expression of fibulin-2, a novel
A:Reference number: A49457; MUID:94064787; PMID:8245130
A:Accession: A49457
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A;Cross: references: GDB:278285; OMIM:135820
A;Map position: 22q13.3-22q13.3
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; glycoprotein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-683/Product: fibulin I splice form C #status predicted <MAT>
F;180-214/Domain: EGF homology <EGFP>
F;485-523/Domain: EGF homology <EGFI>
F;98,535,539/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                          A; Molecule type: mRNA
A; Residues: 1-1221 <PAN>
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Best Local :
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157; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DECSF -- SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC
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                                                                                                                                                                                                                                                                                                                                                  TVKMDLSRHGTVSSFVAKLFIFVS
                                                                                                                                                                                                                                                                                                                                                                                                              VVFRMGPSSAVPGDSMQLAITGGNEEGFFTTRKVSPHSGVVALTKPVPEPRDL-----LL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel protein that interacts with the fibronectin receptor beta-subu A32826; MUID:89354537; PMID:2527614
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Pred. No. 4.1e-41;
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A; Note: DKFZp586A1519.1
C; Superfamily: fibulin-2; EGF homology
C; Keywords: alternative splicing; extracellular matrix
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-1184/Product: fibulin-2 protein #status predicted
                                                                                                                                     A; Experimental
C; Genetics:
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fibulin-2 precursor - human

N;Alternate names: protein DKFZp586A1519.1

C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02
C;Accession: A55184; T08744

R;Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Ch
Genomics 22, 425-430, 1994
A;Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression,
A;Reference number: A55184; MUID:95104855; PMID:7806230
                                                                                                                           A;Molecule type: mrNA
A;Residues: 656-719,'QDECLMGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCVD',720-853,'T',855
A;Cross-references: EMBL:AL050095
A;Gene: GDB:FBLN2
A;Cross-references: GDB:2
A;Map position: 3p25-3p24
                                                                                                                                                                                                                      A;Cross-references: GB:X82494; NID:g575232; PIDN:CAA57876.1; R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wissubmitted to the Protein Sequence Database, March 1999 A;Reference number: Z16471 A;Accession: T08744
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A;Accession: $74095
A;Molecule type: protein
C;Superfamily: fibulin-2; EGF homology
C;Superfamily: fibulin-2; EGF homology
C;Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; hor E;942-978/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1184 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: A55184
                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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146; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-RFDCPPNYVRVSQTKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAG
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                                                                                                               source: adult uterus;
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                            GDB:293037;
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Pred. No. 1.2e-40;
0; Mismatches 149
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                                                                                                            clone DKFZp586A1519
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N; Alternate names: basement membrane protein BM-90
C; Species: Mus musculus (house mouse)
C; Date: 24-Jul-1998 **sequence_revision 24-Jul-1998 **text_change 02-J
C; Accession: $78040; $78560; $36440
R; Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L
Eur. J. Biochem. 215, 733-740, 1993
A; Title: Sequence of extracellular mouse protein BM-90/fibulin and :
A; Reference number: $34968; MUID:93358897; PMID:8354280
A; Accession: $78040
A; Molecule type: mRNA
A; Residues: 1-685 < PANY
A; Cross-references: EMBL:X70854
R; Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L
submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular protein - human
(;Species: Homo sapiens (man))
(;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: I38449
R;Lecka-Czernik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1955
A;Title: An overexpressed gene transcript in senescent and quies
A;Reference number: I38449; MUID:95097983; PMID:7799918
A;Accession: I38449
A;Accession: A;Accession: I
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$78040
fibulin, splice form C precursor - mouse
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A;Gene: S1-5
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Pred. No. 3.4e-56;
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N;Alternate names: fibulin C
N;Contains: fibulin 1 splice form A; fibulin 1 splice form C
C;Species: Homo sapiens (man)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
C;Accession: C36346; A36346; A32826
C;Accession: C36346; A36346; A36826 W H: Dickerson, K.
                                                                                                                                                                                        C;Accession: C36346; A36346; A32826
R;Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K
J. Cell Biol. 111, 3155-3164, 1990
A;Title: Fibulin is an extracellular matrix and plasma A;Reference number: A36346; MUID:91100426; PMID:2269669
A;Accession: C36346
A;Cross-references: GB:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415 R;Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E. Cell 58, 623-629, 1989
                                                                                                        A;Residues: 1-683 </br>
A;Cross-references:<br/>A;Accession: A36346
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C;Keywords: alternative splicing; basement membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-39, 'P', 41-685 <CHU>
A; Cross-references: EMBL: X70854
                                                              A; Molecule type: mRNA
A; Residues: 1-566 < AR
                                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                           fibulin 1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                   precursor, splice form C -
te names: fibulin C
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                                                            1-566 <AR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECSF - - SEFICQHECVNQPGTYFCSCP - PGYILLDDNRSCQDINECEHRNHTCNLQQTC
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Pred. No. 1.1e-41;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 3, 2003, 17:36:12; Search time 18.0023 Seconds
(without alignments)
2392.374 Million cell updates/sec

Title:
US-09-674-379A-13
Sequence:
2533
Sequence:
1 MPGIKRILTVTILALCLPSP......INFRGSSVIRLRIYVSQYPF 448
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:
283224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	Ø	υ	4	ω	2	_	NO.	Result
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Notch-1 protein -	growth potentiatin	notch homolog – se	notch protein homo	notch 3 protein -	growth arrest-spec	notch3 protein - h	Xotch protein - Af	fibropellin Ia – s	transmembrane prot	notch protein - fr	notch protein homo	hypothetical prote	notch4 - mouse	receptor tyrosine	Nel-homolog protei

## ALIGNMENTS

poldermal growth factor-like protein, 716 precursor - ratt C;Species; Rattus norvegicus (Norway rat) C;Accession: JC5621 A;Reference number: JC5621; MUD:97415782; PMID:9268694 A;Reference number: JC5621; MUD:97415782; PMID:9268694 A;Reference number: JC5621; MUD:97415782; PMID:9268694 A;Residues: 1-493 - OXA- A;Residues: 1-4								
owth factor-like protein, T16 precursor - rat attus norvegicus (Norway rat) protein, T16 precursor - rat attus norvegicus (Norway rat) protein protein, T16 precursor - rat ct-1997 *sequence_revision 07 Nov-1997 *text_change graction of DA41, a DAN-binding protein, with the ep number: JC5621; MUID:97415782; PMID:9268694  JC5621 JC5621; MUID:97415782; PMID:9268694  JC5621; MUID:9741583; JP-926; PMID:9268694  JC5621; MUID:9741589782; PMID:9268694  JC5621; MUID:9741589782; PMID:9268694  JC5621; MUID:9741589782; PMID:9268694  JC5621; MUID:9741589739; NID:9242982; PMID:926871 predict  JC5621; MUID:9741589739; NID:9242982; PMID:926872; PMI							Query Matc Best Local Matches 2	RESULT 1 JC5621 epidermal gr C;Species: R C;Species: 09-0 C;Accession: R;Ozaki, T.;
05-NOV-1999 A.; Sakiyama, S. idermal growth facto idermal growth facto piD:d1023127; piD:g2 rowth by interacting 1 growth factor-like ted 93; 47; Gaps 5; MMCVNONGGY 66	EPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFOMQATTRYPGAYYIF :  :  :  :	CVNOPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDDIRCE	GRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHE:  :  ;   :    :    :    :    :    :	EVQTGRNNFVIRRNPADPQRIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQ ICINTEGGYTCSCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNED	LCIPRTNPVYRGPYSNPYSTPYS	ILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGY :  :::	43.8%; Score 1109.5; DB 2; Length 493; Similarity 42.3%; Pred. No. 1.1e-65; 6; Conservative 73; Mismatches 161; Indels 47; Gaps	ctor-like protein, T16 precursor - rat orvegicus (Norway rat) #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999  K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, es. Commun. 237, 245-250, 1997  n of DA41, a DAN-binding protein, with the epidermal growtl JC5621; MUID:97415782; pMID:9268694  NA OZA> DDBJ:D89730; NID:92429082; PIDN:BAA22265.1; PID:d1023127; tein plays a role in the regulation of cell growth by inter otein al sequence #status predicted <sig> -237,238-277,278-318,319-359/Region: epidermal growth facto carbohydrate (Asn) (covalent) #status predicted</sig>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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N-PSDB; AAZ39386, AAZ39387.
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Pred. No. 2.5e-153;
9; Mismatches 13;
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This sequence is the mouse A55 protein. The invention relates to human A55 protein. The protein can be used for the treatment of due to abnormal proliferation of smooth muscule. The polypeptides used according their inhibition of the proliferation of vascular
                                                                                                                                                                                                                                              A55 protein; mouse; smooth muscle proliferation; tissue generation; vascular smooth muscle cell; arterlosclerosis; tissue reparation; m vascular endothelial thickening; haematopoietic cell-regulator; cyt percutaneous transluminal coronary angioplasty; blood coagulation; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
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DB; AAZ40029.
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                                                                                                                                  Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
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Pred. No. 2.4e-153;
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28-APR-1998; 28-APR-1999; 04-NOV-1999.

98JP-0119731 99WO-JP02283

22-FEB-2000

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadohelin/tumour metastasis inhibiting activity tumor inhibition, and as nutrient. The present sequence represents the mature protein of the invention which can be used for modulating smooth muscle cell proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 63-65; 70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell proliferation; vascular; smooth muscle cell; arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ONOY ) ONO PHARM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-038646/03
DB; AAZ39388.
                                                                                                         181
301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
                                    241
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                                                                                                                                                                                                                                                                                                                                                                                           401;
                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                  61 TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
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                                                                                                                      QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
                                                                                                                                                                                             NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
                                                                                                                                                                                                                                                                                                                  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                     QDVNECETENPCVQTCVNTYGSFICRCDPGYELEEDGIHCSDMDECSFSEFLCQHECVNQ
                               PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 300
                                                                                                                                                                           NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNDDGRSC
                                                                                                                                                                                                                                               TSYSGPYPAAAPPVPASNYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHQCNPTQICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tashiro K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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94.8%;
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QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS

QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS

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                                                                                                 The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cand coagulation/thrombotic activity; tumor inhibition, and as nutrient. The present sequence represents the protein of the invention which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                           Sequence
                                                                                                                                                                                                                                                                                                      Claim 1; Page 42-44; 70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smooth muscle proliferation modulating protein.
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                                                                                                                                                                                                                                                                                                                                                  Novel mouse polypeptides for treatment, e.g. arteriosclerosis and myoma
                                                                                                                                                                                                                                                                                                                                                                                                                          Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1998;
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 401;
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 AAZ39384.
                                                                                         smooth muscle cell proliferation.
               95.68;
94.88;
                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura
 9;
Score 2302; DB 21;
Pred. No. 2.4e-153;
9; Mismatches 13;
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   Indels
                             Length
                               448;
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RESULT 11
AAY56751*
ID AAY56
XX AAY56
XX AAY56
XX AAY56
XX SMOOT
XX Cell
CH Coll
KW Cell
KW endot
KW myoma
KW actir
KW myoma
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KW myoma
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Best Local
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                                                                                                                         Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA endothelial thickening; percutaneous transuluminal coronary angioplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
              28-APR-1999;
                                                                                            Mus musculus
                                                                                                                       metastasis; nutrient.
                                                                                                                                                                                           Smooth muscle proliferation modulating protein mature
                                                                                                                                                                                                                              22-FEB-2000
                                                                                                                                                                                                                                                         AAY56751;
                                                                                                                                                                                                                                                                               AAY56751 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polypucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides are useful in the recombinant production of the homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polypuclectides can also be used in gene therapy e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace a defective gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
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           99WO-JP02283
                                                                                                                                                                                                                                                                               Protein;
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Pred. No. 2.8e-160;
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                                                                                                                                         taxis;
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RESULT 12
AAY56753
ID AAY56
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AC AAY56
XX

AAY56753 standard;

Protein;

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AAY56753

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel mouse polypeptides for treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Honjo
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421
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                                                                                                                                                                                                                                                                            61 TSYSGPYPAAAPPVPASNYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHQCNPTQICI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page
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                                      ΥPF
                       YPF
                                                                                    LIGENRCMCPAEHTSCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                                                  RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                                                                                               PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCJDPIRCEEPYL
                                                                                                                                                                                QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                            NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
                                                                                                                                  PGSYFCSCPPGYVLLDDNRSCQDINECEHRNHTCTSLQTCYNLQGGFKCIDPISCEEPYL
                                                                                                                                                                                                                                                                                                                        QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                                                                                                                                                                        TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tashiro K,
                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA;
                     423
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51-53; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0119731
                                                                                                                                                                                                                                                                                                                                                                                     95.6%;
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                                                                                                                                                                                                                                                                                                                                                                         Score 2302; D
Pred. No. 2.2e
9; Mismatches
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2.2e-153;
es 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183; PRO185; PRO210; PRO217; PRO244; PRO288; PRO365; PRO1301; PRO130 PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318; PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356; PRO246; PRO941; PRO941; PRO1096; PRO6003; PRO6004; PRO350; PRO2630; PRO246; PRO265; PRO941; PRO1096; PRO6003; PRO6004; PRO350; PRO2630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
 Modified-site
                                                  Modified-site
                                                                                                               Homo sapiens.
                                                                                                                                                                                                                           Amino acid sequence of human polypeptide PRO210.
                                                                                                                                                                                                                                                                                                        AAB31183 standard;
                                                                          Peptide
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                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                    death; genetic disorder; transgenic animal; gene therapy
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                      /note-
21..27
/note-
54..57
/note=
64..70
                                                                         Location/Qualifiers
1..25
                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%;
          "cell attachment site"
                                  "N-myristoylation site"
                                                           "signal peptide"
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Pred. No. 2.8e-160;
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01-SEP-1999

08-SEP-1999

15-SEP-1999

15-SEP-1999

30-NOV-1999

01-DEC-1999

07-DEC-1999

07-DE
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20-JUL-1999;
26-JUL-1999;
17-AUG-1999;
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(GETH )
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GENENTECH INC.
                                                                99US-0169495
2000WO-US00219
2000WO-US04341
2000WO-US04414
2000WO-US05601
2000WO-US05601
2000WO-US05841
2000WO-US05841
2000WO-US05841
2000WO-US05843
2000WO-US033358
2000WO-US13358
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99WO-US28565
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99WO-US20111.
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99US-0145070
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296..300
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283..287
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267..273
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242..248
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226..232
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Ashkenazi AJ, b...
Porrara N, Fong S, Gav
Stewa Zhang Baker KP, L. Geru. S, Gao W, Geru. Kljavin J Botstein DA, W, Gerber H, Kljavin IJ, Tumas Desnoyers L, Eaton D Gerritsen ME, Goddar Mather JP, Napier MA, D, Watanabe CK, Will Eaton DL; Goddard A; c MA, Pan J; Williams PM; Pan

N-PSDB; 2001-050091/06. DB; AAC86968.

Isolated nucleic acid molecule encoding transmembrane polypeptide is useful for of related polypeptides a PRO polypeptide which is gene therapy and identifica identification

Claim 12; Fig 10; 244pp; English.

The present sequence represents a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated pR0196, pR0444, pR0183, pR0185, pR0210, pR0215, pR0217, pR0242, pR0286, pR0365, pR01361, PR01183, PR01272, pR0419, pR04999, PR07170, pR0248, pR0353, pR01318, pR01600, pR09940, pR0533, PR0301, pR0187, pR0337, pR01411, pR04356, pR0246, pR0265, pR0941, pR010096, pR06003, pR06004, pR0350, pR02630 and pR06309. The biological activity of cells

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CC Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic CC thyroiditis), diabetes mellitus, immune-mediated renal disease CC (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis, CC (idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune CC (hepatitis, and sclerosing cholangitis, inflammatory bowel disease CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and CC (ulcerative colitis: thin a multiforme contact dermatitis, psoriasis, CC (urticaria, ecsinophilic pneumonia, idiopathic pulmonary fibrosis, CC urticaria, ecsinophilic pneumonia, idiopathic pulmonary fibrosis, CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists CC (antibodies against (I) can also be used for diagnosing such diseases. CC Antibodies against (I) can also be used for diagnosing such diseases. CC This sequence represents a human EGF-like homologue encoded by cDNA clone xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 422;
PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                18-DEC-2001
                                                                                                                          AAU29227
                                                                                                                                                AAU29227 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                        QDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
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                                                                      polypeptide
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                                                                                             (first entry)
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                                                                     sequence #204.
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Pred. No. 2.8e-160;
0; Mismatches 1;
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2000US-198121P
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ŗ c KP, Chen J J, Smith V, ٦ Watanabe CK, 1 , Goddard A, Godowski pJ, Wood WI, Zhang Z; Gurney

N-PSDB; 2001-602746/68. DB; AAS46128.

Novel nucleic acids encoding PRO polypeptides, used to dispresence of tumours, such as prostate and breast tumours, to screen for modulators of the compounds diagnose the rs, in mammals and

Claim 11; Fig 408; 774pp; English.

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate animal

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AIDS) related dementia, ocular disorders, kidney disorders, liver disorders, hair follicle growth promotion, burns, ulcers, corneal inflammation, neoplasms and psoriasis), to raiss specific antibodies and to characterise receptors. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            least 95% identical with a sequence (ATCC 97285) encoding mature human extracellular protein-like/epidermal growth factor (EGF)-like protein, EEGF. Also included are the EEGF EGF domains, a vector containing the polynucleotide, a host cell containing the vector, anti-EEGF antibodies and antagonists of EEGF. The polynucleotide is used for recombinant production of EEGF, in gene therapy, as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel polynucleotide which is at least 95% identical with a sequence (ATCC 97285) encoding m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen HS,
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10-APR-1996;
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(LIHH/) LI H.
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                                                                                                                                                                                                        PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
                                                       RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
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                                                                                                                                                                            PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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96WO-US05247
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28-OCT-1997;
12-NOV-1997;
21-NOV-1997;
24-NOV-1997;
Sjogren's syndrome, systemic vascuitor, paroxysmal hemolytic anemia (immune pancytopenia, paroxysmal hemoglobinuria), autoimmune thrombocytopenia (idio hemoglobinuria), autoimmune thrombocytopenia), thyroid
                                                                                             This invention describes a novel composition containing (apart from a carrier or exciplent), a novel PRC245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune related diseases, particularly T cell-mediated diseases. The diseases treated include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; diopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
                                               arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune
                                                                                                                                                                                                                                                                                           Example 1;
                                                                                                                                                                                                                                                                                                                         antagonist
                                                                                                                                                                                                                                                                                                                                           Composition containing novel polypeptide PRO245, its
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-229499/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1998;
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                                                                                                                                                                                                                                                                                      Fig
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970S-0059263.
970S-0063550.
970S-0065186.
970S-0066364.
970S-0066770.
980S-0088026.
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                                                                                                                                                                                                                                                                                      177pp;
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                                                                                                                                                               clones. 830 cDNA molecules encoding a human protein have been 1solated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primers for synthesising full length
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing use in genetic manipulation -
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N-PSDB; AAK94505.
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                                                                                                                                                    GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
                                                                                                                                                                                                                                                                                                        PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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Pred. No. 1.1e-160;
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Best Local Similarity
Matches 423; Conser
                                                                                                                                                                                                                                                                                                                                                       This sequence is the human A55 protein of the invention. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actino/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadherin/tumour metastasis inhibiting activity; tumour inhibition, and as a nutrient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A55 protein; human; smooth muscle proliferation; tissue generation; vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma; vascular endothelial thickening; haematopoietic cell-regulator; cytokine; percutaneous transluminal coronary angioplasty; blood coagulation; PTCA; actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 76-80;
                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides
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                                           QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
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         cells containing a vector comprising the ECMP-1 nucleic acid ar for the recombinant production of the protein. ECMP-1 and its (ant)agonists, are useful in the diagnosis, prevention, and tre of cancer and immune disorders.
 Sequence
                                                         Claim 1;
                                                                     New polynucleotide encoding useful in the diagnosis, predisorders and cancer
                                                                                                                                                                              07-JAN-1999
                                                                                                                                                                                                                                         Human extracellular matrix protein (ECMP)-1.
                                                                                                                                    (INCY-) INCYTE PHARM
                                                                                                                                                   27-JUN-1997;
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DB; AAX05359.
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                                                                           ing extracellular matrix protein, Enterprevention and treatment of immune
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                                                                                              Jacobs K,
Agostino I
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21-MAY-1998;
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Pred. No. 1.1e-160;
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Matches 423;
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N-PSDB; AAV62432.
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                         PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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Matches 423
                                                                                                                                                                                                                The sequence is that of a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
                                                                                                                                Sequence
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N-PSDB; AAX07567.
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution being printed,

1 2 3 4 4 4 6 6 7 7 10	Result No.
2407 2407 2407 2407 2407 2407 2401 2401	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
44444444444444444444444444444444444444	Length DB
20 20 21 22 23 23 23	DB:
AAW79739 AAW95709 AAW95709 AAW54081 AAW57086 AAW54989 AAW93573 AAU75494 AAW93573 AAU75494 AAW93573 AAU29227 AAW29237	ID
Human EEGF protein Homo sapiens fetal Human extracellula Amino acid sequenc Full length human Human polypeptide, Human extracellula Human FGF-like hom Human PRO polypept Amino acid sequenc	Description

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735.5	735.5	811.5	811.5	811.5	912.5	912.5	912.5	963.5	963.5	989.5	992.5	1093.5	1093.5	1106	٠	٠	1272.5		•		•		1276.5	6	1827	1827	1827	2230	2302	2302	2302	2302	2302	2302
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18	12	22	23	22	23	22	21	22	20	21	21	22	22	22	21	22	21	23	22	21	21	21	20	18	23	22	21	18	21	21	21	21	21	21
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ulin typ	lin c	iat	Human albumin fusi	ted prote	~		Human EGF extracel	ellular p	Human EGF-like pro	minal of p	-terminal	extracell		<b>-</b>	C	Human protein sequ	m.	PRO226	poly			Human PRO226 prote	Extracellular prot	n extracellul	Rat protein isolat	-	Rat EGF extracellu	_	length mc		ength mo	muscle	muscle	Smooth muscle prol

## ALIGNMENTS

AAW79739 standard; Protein; 448

AA.

25-JAN-1999 AAW79739;

·(first entry)

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RESULT 1
AAW79739
ID AAW79739
AC AAW7
XX AAWT
AC AAW7
XX Extr
DE Huma
AX Extr
CW Extr
CW Wour
KW Wasc
KW Wour
KW Wour
KW Wour
KW Wour
KW Wour
KW Wour
KW Home
XX Home

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human EEGF protein.
Region
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112..153
                                      191..230
/label= EGF-3
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/note= "Extracellular/epidermal
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26..448
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1251 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02251-3
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885 -----GCEEVEOP 892
                         310 PAENPGCR--DQP 320
                                           833 LGHRLVGGRKCKKDIDECSQDPGLC-LPHACENLQGSYVCV----CDEGFTLTQDQH---- 884
                                                             250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 309
                                                                                               654 FCINFPGHYKCNCYPGYRLKASRPPICEDIDECRDPSTCPDGKCENKPGSFKCIACQPGY 713
                                                                                                                                                                                                                        621 ------KCNRGYRLHVGAGGRSCVDLNECA-KPHLCGDGG 653
                                                                                                                                                                                                                                                                                                                 61 TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD---ESNQCVDVDECATDSHQCNPTQ 117
                                                                                                                                                                                                                                                                                                                                       2 CTNGFDLDRQSGQCLDIDECRTIPEAG-RGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
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earch completed: July 3, 2003, 18:26:54 (ob time : 13.1125 secs

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PCT-US95-02251-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application PC/TUS9502251 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE: 30-SEP-
                                                                                                                                                                                                                                                                           SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
CLASSIFICATION:
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC009P--
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                              CLASSIFICATION: US 0 APPLICATION NUMBER: US 0 FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Vers
SOFTWARE: #1.30
   TELEX:
                     TELEFAX:
                                    TELEPHONE:
                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
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                     789-2679
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                                                                                                                                                                                     US 08/199,780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9502251 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 117;
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                                                                                                                                                                                                                                                           SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                   APPLICATION NUMBER: PCT/UIFILING DATE: CONCURRENTLY CLASSIFICATION:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
                                                                       CLASSIFICATION:
                                                                                         APPLICATION NUMBER: FILING DATE: 18-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                 NAME: Parker, David L. REGISTRATION NUMBER: 32,165
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 -HTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC------PAENPGC 316
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                                                                                                                                                                                                                                                                                                                                                                                           77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECDRGYIMVRK-GHCQDINECRH-PGTC-PDGRCVNSPGSYTCL-ACEEGYVGQSGSCVD 102:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.O.
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                                                                                          18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHODS AND COMPOSITIONS FOR STIMULATING BONE CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%; Score 453; DB 5; 33.1%; Pred. No. 1.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White
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                                                                                                            US 08/199,780
                                                                                                                                                                                                                        PCT/US95/02251
RENTLY HEREWITH
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UMIC009P--
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RESULT 12
US-08-897-443-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linea
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 638 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shah, purvi
APPLICANT: Kaser, Mathew
TITLE OF INVENTION: HUMAN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
    Local Similarity
                                                              LIBRARY: UTRSNOT02
CLONE: 681719
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94304
                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
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                                                                                                                                              638 amino acids
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                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
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                                                                                                                 single
   18.98;
28.18;
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                                                                                                                                                                                                                                  PF-0348 US
Score 455; DB 2;
Pred. No. 2.7e-28;
            Length 638;
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US-08-479-722B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08479722B Patent No. 6074840
                                     TELEFAX: (713) 934-7011 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                            FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/199,780

FILING DATE: 18-FEB-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 30-SEP-1994
                  SEQUENCE CHARACTERISTICS
                                                                     REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 934-7000
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: LA TITLE OF INVENTION: GE NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bonadio, Jeffrey APPLICANT: Yin, Wushan
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 77040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 CFEGYILREDGKTCRRKDVCQAIDHGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TPYSGPYPAAAPPLSAPNYPTISRPLICREGYQMD-ESNQCVDVDECATDSHQCNPTQIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                           Fussey, Shelley P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEEPYLRISDNR-C----MCPAENPGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas
1833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Williams, Morgan & Amerson
7676 Hillmont, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995
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                                                                                                                                                                                                                                                     US 08/316,650
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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ADDRESSEE:

3174 Porter Drive

Incyte Pharmaceuticals,

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RESULT 10
US-09-188-930-336
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               Sequence 336, Application Patent No. 6150502
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,168
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LENGTH: 387 amino acids
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IMMEDIATE SOURCE:
LIBRARY: GenBa
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MEDIUM TYPE: Diskett
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
                                                                                                                                                                                                                                                                                                                                                                                      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC
                                                                                                              RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
||| |:|| ||: : |||| :||::: || |||:|| | | |
RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                   PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM
                                                                                                                                                                                                                                                                      NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP
                                                                                                                                                                                 PVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL
                                                                                                                                                                                                                                                 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC
                                                                                                                                                                                                                                                                                                                                                     NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCP 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADPORTPSNP -- SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC
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                                 US/09188930A
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5177197-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Patent No. 5177197; APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;; WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-188-930-336
                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENA; HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 336 LENGTH: 274
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE OF INVENTION: and Methods For Their Use
FILE APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION UNDEER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: OS APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-FEB-1990 NO:30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
105 ECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGYCQQ-LCANVPG
                                                               615 -CPAGFMASEEGTNCIDVDECLRPDVCGEGHCVNTVGAFRCEYCDSGYRMTQRGRCEDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TITSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SGAHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNPLCREQPSSIVHRYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 PGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD
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                                                                                                         PYSGPYPAAAPPLSAPNYPTISRPLI---
                                                                                                                                                CYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSFLCI---
                                                                                                                                                                                      CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                     22.4%;
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                                                                                                                                                                                                                               ; Score 539; DB 6; Length 1394; ; Pred. No. 1.5e-34; 51; Mismatches 126; Indels 122;
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Pred. No. 8e
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73;
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                                                                                                         --- CRFGYQMDESNQCVDVD 104
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

Rockville ₹

20850

APPLICATION NUMBER: US/0 FILING DATE: 11-APR-1997

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Sequence 3, Application US/08980514
Patent No. 6004753
GENERAL INFORMATION:
                                                      TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING LALION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/05033
APPLICATION NUMBER: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  370 RQTGPISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
                                                                                                                                                                                                                                                                                                                                                                                    216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 NOCAOOCYNILGSFICOCNOGYELSSDRLNCEDIDECRTSSYLCOYOCVNEPGKFSCMCP
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                                                                                                                                                                                                                                                     ROTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLSAPNYPTISRPLICRFGYOMDESNOCVDVDECATDSHOCNPTQICINTEGGYTCSC 130
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Pred. No. 1.1e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 387;
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                                                                                                                           RESULT 9
US-09-212-168-5
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   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN E.
                                                                                         Sequence 5, Application US/09212168 Patent No. 6303765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acid:
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LIBRARY: GenBar
CLONE: 458228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/980,514
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171; Conservative
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Similarity 48.3%;
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HUMAN EXTRACELLULAR MATRIX PROTEINS
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US-08-980-514-3

334

NUMBER OF SEQUENCES: 3

APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi

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> 38 71

; MOLECULE TYPE: protein US-08-833-963C-9

TOPOLOGY:

linear single

TYPE: amino acid STRANDEDNESS: Sir

Query Match 40.0 Best Local Similarity 48.3 Matches 171; Conservative

40.0%;

TELEFAX: 301-30. 9:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FRIGTH: 387 amino acids

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US-08-884-072-5
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bandmar
APPLICANT: Corley,
APPLICANT: Guegle:
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                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: BRSTN
CLONE: 2786449
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LENGTH: 443 amino acid
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                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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COUNTRY:
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REGISTRATION NUMBER: 36
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                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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                                                                                                           Sequence 9, Application US/08833963C Patent No. 5916769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
GENERAL INFORMATION:
APPLICANT: Olsen, et al.
TITLE OF INVENTION: Extracell
TITLE OF INVENTION: HCABA58X
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY ATT
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LIBRARY: GenBa
CLONE: 458228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                        370 RQTGPISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                      156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
                                                                                                                                                                                                                                                                                          274 PVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL
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Similarity 48.3%;
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Pred. No. 1.1e-68;
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Mismatches 123;
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ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Ave

Extracellular/Epidermal Growth

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US-08-833-963C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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NAME/KEY: UNSURE
LOCATION: (167)...(167)
NAME/KEY: UNSURE
LOCATION: (183)...(183)
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LOCATION:
NAME/KEY:
                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                          FILING DATE: 10-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Extracellular/Epidermal Growth Factor TITLE OF INVENTION: HCABA58X
                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 208
                                                                                                                   APPLICATION NUMBER: US/08/833,963C FILING DATE: 11-APR-1997 CLASSIFICATION: 435
                            NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                             STREET: 9410 Ke
CITY: Rockville
                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  STATE:
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o. 5916769
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9410 Key West Ave
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                                                                                                                                                                                                                      Floppy disk
                                                                           JMBER: WO PCT/US96/05033
10-APR-1996
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93.78;
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Pred. No. 4
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ches 15;
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; MOLECULE TYPE: protein US-08-833-963C-2
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US-08-980-514-1
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                                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 6004753 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                    APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                   COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                   ADDRESSEE: inc.
APPLICATION NUMBER: US/08/9 FILING DATE: Filed Herewith
                                                                                                                                                              STREET: 3174 PO:
CITY: Palo Alto
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                                                                                       MEDIUM TYPE:
                                                                                                                                    COUNTRY:
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            US/08/980,514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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360 320 300 240 201

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PRIOR APPLICATION DATA:

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US-09-212-168-1
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   INFORMATION FOR
                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                   TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: P
STATE:
                     TELEFAX:
TELEX:
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 YPF 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 3174 Porter Drive
                                       415-845-4166
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   SEQ
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                                                                                  SEQ ID NO 186
LENGTH: 337
TYPE: PRT
ORGANISM: Rat
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Matches
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                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                      APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011C1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                       NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
NAME/KEY: UNSURE
LOCATION: (14)...(124)
NAME/KEY: UNSURE
LOCATION: (135)...(135)
                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: CORNN
CLONE: 45517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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Pred. No. 1.4e-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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385 360 325 300 240 205 180

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Minimum DB:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           1276.5
1276.5
963.5
963.5
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US-08-199-780-3
US-08-479-722B-4
US-08-897-443-3
US-08-897-110-116-3
US-08-99-110-116-3
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US-08-980-514-1

US-08-833-963C-9

US-08-884-072-5

US-08-833-963C-9

US-08-980-514-3

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US-08-884-072-1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN E
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                TELEX:
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
340.5	340.5	340.5	342.5	342.5	345.5	345.5	350.5	351.5	351.5	354.5	361.5	361.5	361.5	361.5	361.5	369	369
14.1	14.1	14.1	14.2	14.2	14.4	14.4	14.6	14.6	14.6	14.7	15.0	15.0	15.0	15.0	15.0	15.3	15.3
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Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 17, Appl	20,	20,	Sequence 2, Appli	Sequence 4, Appl:	Sequence 19, Appl	Sequence 1, Appli	Sequence 37, Appl	Sequence 37, Appl	`	Sequence 37, Appl	Sequence 37, Appl	Sequence 1, Appl	Sequence 19, Appl

## ALIGNMENTS

US/08884072

HUMAN EXTRACELLULAR MATRIX PROTEINS

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; CLONE:
US-08-884-072-1
                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US, FILING DATE: Herewith CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                 TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 PORT
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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CLONE: 45517
                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                  LENGTH: 448 amino acids
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3174 Porter Drive
                                                                                   CORNNOTO
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2407; DB 2;
No. 1.4e-182;
               Length 448;
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                                                                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Cben, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin I
APPLICANT: Pan, James
Prior Application removed - See file Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
TYPE: PRT
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Sequence 408, Application US/10176913 Publication No. US20030022298A1
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APPLICANT:
APPLICANT:
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LENGTH: 448
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                                                                        CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILLING DATE: 2002-66-20
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                           Smith, Victoria Watanabe, Colin K. Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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; ORGANISM: Homo Sapien US-10-180-552-408
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; Sequence 408, Application US/10180552
; Publication No. US20030022300A1
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Query Match
Best Local Similarity 99.8
Matches 422; Conservative
                                                                                   CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapp NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
TYPE: PRT
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Best Local
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C153
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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APPLICANT:
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Godowski, Paul
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     Score 2401; DB 9;
Pred. No. 2.3e-159;
0; Mismatches 1;
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RESULT 12
US-10-176-482-408
US-10-176-482-408
; Sequence 408, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
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APPLICANT:
APPLICANT:
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-10-175-752-408
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 2.3e-159;
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RESULT 13
US-10-176-757-408
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
                                                                                                                                                                                                                             Sequence 408, A Publication No.
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Best Local Similarity
Matches 422; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
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APPLICANT:
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C86
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ORGANISM: Homo Sapien
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                       Smith, Victoria Watanabe, Colin Wood, William I.
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                                                                                                         Pan, James
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    See File

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Pred. No. 2.3e-159;
0; Mismatches 1;
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Sequence 408, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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US-10-173-706-408
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9439R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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                                                          GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
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Smith, Victoria
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RESULT 11
US-10-175-752-408
; Sequence 408, Application US/10175752
; Publication No. US20030022295A1
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; ORGANISM: Homo US-10-175-738-408
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US-10-175-738-408
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
TYPE: PRT
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APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
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                       YPF 423
                                                GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
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Pan, James
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Goddard, Audrey
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Pred. No. 2.3e-159;
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ORGANISM: Homo Sapien
IS-10-176-758-408
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 408
LENGTH: 448
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CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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US-10-175-737-408
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
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Best Local :
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LENGTH: 448
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P9430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
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Pred. No. 2.3e-159;
0; Mismatches 1;
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APPLICATION NUMBER: PCT/US98/25108
FILING DATE: 1998-12-01
APPLICATION NUMBER: PCT/US98/25190
FILING DATE: 1998-11-25
                                                                                                                                           APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
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FILING DATE: 1998-09-16
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APPLICATION NUMBER: PCT
FILING DATE: 1998-09-14
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APPLICATION NUMBER: PCT/US98/24855
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FILING DATE: 2001-06-19
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FILING DATE: 2001-05-30
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FILING DATE: 2001-01-22
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Pred. No. 2.3e-159;
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Publication No.
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
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OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/66840
OR FILING DATE: 1997-11-25
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR FILING DATE: 1998-02-09
OR FILING DATE: 1998-02-09
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APPLICATION NUMBER: 60/059115
FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
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FILING DATE:
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FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063329
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FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059588
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Timothy A. Stewart
Daniel Tumas
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A. Botstein
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            DR FILING DATE: 1999-03-05

PR APPLICATION NUMBER: 09/284663

PR FILING DATE: 1999-04-15

PR APPLICATION NUMBER: 09/332928

PR FILING DATE: 1999-06-14

PR FILING DATE: 1999-06-14
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101922
FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/106032
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APPLICATION NUMBER: 60/109304
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APPLICATION NUMBER: 60/125778
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FILING DATE: 1999-03-09
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DR APPLICATION NUMBER: 60/095998
DR FILING DATE: 1998-08-10
DR APPLICATION NUMBER: 60/097000
DR FILING DATE: 1998-08-18
DR APPLICATION NUMBER: 60/099601
DR FILING DATE: 1998-09-09 APPLICATION NUMBER: 60/099803 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099811 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 1998-04-08 60/099803 60/081049

1998-09-10 60/099812

OR FILING DATE: 1999-07-26

OR APPLICATION NUMBER: 60/149396

OR FILING DATE: 1999-08-17

OR APPLICATION NUMBER: 60/169495

OR FILING DATE: 1999-12-07

OR APPLICATION NUMBER: 08/918874

OR FILING DATE: 1997-08-26 1997 -09-19 1999-07-20 1999-03-23 08/960507 08/933821 60/145698 60/145070 60/139695

FILING DATE: 1998-08-19
APPLICATION NUMBER: 09/136804
FILING DATE: 1998-08-19
APPLICATION NUMBER: 09/136828
FILING DATE: 1998-08-19 APPLICATION NUMBER: 09/114844 09/136801 09/158342

1998-12-08 09/202088 09/180997

APPLICATION NUMBER: 09/254465 09/254460

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RESULT 4
US-09-836-561-1
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Sequence 1, Application US/09836561 Patent No. US20020038006A1
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Best Local :
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 448 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/275,805
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: RC
STATE: N
COUNTRY:
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TYPE: amino acid
TOPOLOGY: linear
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Pred. No. 8.9e-160;
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Best Local S
Matches 423
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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FILING DATE: CUNKNOWNS
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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OPERATING SYSTEM: DOS
SOFTWARE: FRASESE for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
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Corley, Neil C.
Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
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                        301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                              266
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                                                                                                                                                            181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
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                                                                                          241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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                                                                         RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                                                                                           QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
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TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
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llarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                              Sequence 2, Application US/09083002
Patent No. US20010016650A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                APPLICANT: Tashiro, Kei
APPLICANT: Nakamura, Tomoyuki
TITLE OF INVENTION: SECRETED PROTEINS
NUMBER OF SEQUENCES: 2
                                                                        CORRESPONDENCE ADDRESS:
                          STREET: 8/ Cambridge
                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
             COUNTRY:
                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446
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02140
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TYPE: amino acid
STRANDEDNESS: NO. US20020165151A1
                                              87 CambridgePark
             U.S.A.
                                                                                                                                                                          Treacy, Maurice
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Racie, Lisa A.
                                                                                                                                                               Agostino, Michael
                                                                                                                                                                                                Merberg, David
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                                                                                                                                                                                                                                                  Jacobs, Kenneth
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                                                           Genetics Institute,
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Pred. No. 8.9e-160;
Mismatches 0;
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                   RESULT 3
US-09-275-805-2
Sequence 2, Application US/09275805
Patent No. US20010051358A1
GENERAL INFORMATION:
APPLICANT: OLSEN, HENRIK S.
APPLICANT: LI, HAODONG
TITLE OF INVENTION: EXTRACELLULAR
TITLE OF INVENTION: LIKE PROTEIN
UMBER OF SEQUENCES: 11
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TELEFAX: (617) 876-581
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
CORRESPONDENCE
ADDRESSEE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
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             ADDRESS
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) NO: 2:
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AER: P-41,323
GENOME
                     LIKE PROTEIN
                                                EXTRACELLULAR
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SCIENCES,
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                                                EPIDERMAL
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SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        1 QCTINGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                                                                                                                                                                                                  . NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
                    RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
                                                                                                                                                                                PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
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GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
                                                                           RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS
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15, App1
15, App1
15, App1
408, App
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US-10-174-582-408
US-10-175-739-408
US-10-175-739-408
US-10-175-740-408
US-10-176-488-408
US-10-176-488-408
US-10-176-750-408
US-10-176-995-408
US-10-176-991-408
US-10-176-991-408
US-10-176-992-408
US-10-176-993-408
US-10-176-993-408
US-10-176-993-408
US-10-176-993-408
US-10-176-993-408
US-10-173-695-408

Sequence Sequence Sequence Sequence Sequence

Sequence

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/I/pubpaa/U
2: /cgn2_6/ptodata/I/pubpaa/U
2: /cgn2_6/ptodata/I/pubpaa/U
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5: /cgn2_6/ptodata/I/pubpaa/U
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14: /cgn2_6/ptodata/I/pubpaa/I
15: /cgn2_6/ptodata/I/pubpaa/I
16: /cgn2_6/ptodata/I/pubpaa/I
17: /cgn2_6/ptodata/I/pubpaa/I
18: /cgn2_6/ptodata/I/pubpaa/I
19: /cgn2_6/ptodata/I/pubpaa/I
II: /cgn2_6/ptodata/I/pubpaa/I
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length: 2000000000
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Match
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2407
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      : //cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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                US-10-041-016-2
0 US-09-083-002-2
0 US-09-275-805-2
0 US-09-36-561-1
US-10-066-500-15
US-10-176-758-408
US-10-175-737-408
US-10-175-738-408
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US-10-176-757-408
US-10-176-757-408
US-10-173-700-408
US-10-173-700-408
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Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 408, Appli
                                                                                                                                                                                                                                                                                                                  Description
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eing printed,
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US-10-041-016-2
Sequence 2, Application US/10041016
Patent No. US20020165151A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
MCCOY, John M.
                                                                                                                           ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vei

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/041,016

FILING DATE: 07-Jan-2002

CLASSIFICATION: CUMPONNON

PRIOR APPLICATION DATA:
                                   NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
                                                                                 APPLICATION NUMBER: US/09/083,002 FILING DATE: 21-MAR-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED PROTEINS NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
   TELEPHONE: (617)
TELEFAX: (617) 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg, David
Treacy, Maurice
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honjo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LaVallie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCoy, John M.
Racie, Lisa A.
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Zhijian jo, Tasuku

Edward R.

ALIGNMENTS

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Version #1.30

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Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_5.
PROSITE; PS00268; CECROPIN; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_3.
PROSITE; PS01187; EGF_CA; UNKNOWN_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kostka G., Timpl R.;

"Partial sequence of fibulin-6 with a c-terminal region related "Dartial sequence of the fibulin family.";

domain II and III of the fibulin family.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ306906; CAC37630.1; ...

InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, Fibulin-6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-MELANOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MI
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9606;
                                                                                                                                                                                                         2406
2584 ATNQDLIRLVAYTQDGVMHPRTTFLMVDEEQTVPFALRDEN-----
                                                                                                                                   2466 DTCVDIDECENTD-ACQHECKNTFGSYQCICPPGYQLTHNGKTCQDIDECLEQNVHCGPN 2524
                                                                                                                                                                         222
                                                                                                                                                                                                                                                                                                                                             2286 TRGGYKCIDLCPNGMTKAENGTCIDIDECKDGTHQCRYNQICENTRGSYRCVCPRGYRSQ 2345
                                                                                                                                                                                                                                                                                                                                                                                                             2229 QDINECQESSPCHQRCFNAIGSFHCGCEPGYQL-KGRKCMDVNECR--QNVCRPDQHCKN 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2170 CPKGLTIAADGRTCQDIDECALGRHTCHAGQDCDNTIGSYRCVVRCGSGFRRT-SDGLSC
                                                                                                                                                                                                                                                                                                       175 EDGRSCQDVNEC-ATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCS------
                                                                                                                                                                                                                                                                                                                                                               122 TEGGYTC--SCTDGYWLLE-GQCLDIDECRYGYCQ----QLCANVPGGSYSCTCNPGFTLN 174
                                335 SVPADIFQMQATTR----YPGAYYI-----FQIKSGNEGREFYMRQTGPISATLVM 381
                                                                                                                                                                                                                                           222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST
                                                                                                QTCYNLQGGFKCIDPIRCEEPYLRIS-DNRCM--CPAENPGCRDQPFTILYRDMDVVSGR 334
                                                                                                                                                                     ----DMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQ 277
                                                                                                                                                                                                                                                                         GVGRPCMDINECEQVPKPCAHQCSNTPGSFKCICPPGQHLLGDGKSCAGLERLPNYGTQY 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                               PYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICIN 121
                                                                 RMCFNMRGSYQCID-TPCPPNYQRDPVSGFCLKNCPPNDLECALSPYALEYKLVSLPFGI
                                                                                                                                                                                                       SSYNLARFSPVRNNYQPQQHYRQYSHLYSSYSEYRNSRTSLSRTRRTIRKTCPEGSEASH 2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001881; EGF_Ca. IPR003006; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000152; Asx_hydroxyl.
IPR000875; Cecropin.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.5%; Score 542; DB 4; Length 2673; llarity 27.1%; Pred. No. 6.8e-46; Conservative 65; Mismatches 195; Indels 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291017 MW; BEAEC30B8340E272 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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------LKGVVYT 2631
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Qy 382 TRPIKGPR--EIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
|||:::|||:::|||:::||||::
Db 2632 TRPLREAETYRMRVRASSYSANGTIEYQTTFIV--YIAVSAYPY 2673
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Search completed: July 3, 2003, 18:21:58 Job time: 32.0959 secs

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298

CLNTPGSFKCIRTLSCGTGYAMDSETERNNCFLIILNNTFNCKYFFVEDVDECNLGSHDC

-LSAPNYPTISRPLICRFGYQMD---ESNQCV-------DVDECATDSHQC

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Boster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Geubart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Q9VS89;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-JUN-2002 (TrEMBLrel. 21, L
CG7526 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG7526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPTQICINTEGGYTCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLKTTIVGAPNVLPAIRAN-----FLLQKGEKRNSAVVTLRDSLDGPQTVKLQL 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGPREIQLDL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKGSYLCQCPPGYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDECIKFAGHYCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECTTGIAACEQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CTDGYWL--LEGOCLDIDECRYGYCQQL-CANVPGSYSCTCNPGFTLNE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACGLPEE----CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAPNHADTEVNFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --CMCPAENPGCRDQPFTILYRDMDVVSGRSVP-------ADI---FQM
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.7%; Score 547.5; DB 5; Best Local Similarity 32.7%; Pred. No. 8.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0035798; CG7526.

InterPro; IPR000152; Asx_hydroxyl.

InterPro; IPR000561; EGF-1ike.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR003410; Hyalin.

InterPro; IPR000436; Sushi_SCR_CCP.

InterPro; IPR001491; Thrmbomoduln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00032; CCP; 2.

SMART; SM00179; EGF_CA; 9.

SMART; SM00001; EGF_1ike; 5.

PROSITE; PS0010; ASX_HYDROXYL; 8.

PROSITE; PS01186; EGF_CA; 10.

Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;

NON_TER 1394 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 11.
Pfam; PF00084; sushi; 2.
PRINTS; PR00907; THRMBOMODULN.
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003558; AAF50538.1; -. HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
851
                                  313
                                                                                                               263
                                                                                                                                                    737
                                                                                                                                                                                           233
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KTSC
                                  NPGC 316
                                                                                                                                                                        CQHECVNQPGTYFCSCPPGYILLDDNRSCQ
                                                                                                                                                                                                                                                                                                             CQNEPGGFQCACPLGYALSEDMRTCQDIDECLDSNGQCSQLCLNQPGGFACACETGFELT
                                                                                                                                                                                                                                                                                                                                 CINTEGGYTCSCTDGYWLLEGQ--CLDIDEC--RYGYCQQLCANVPGSYSCTCNPGFTLN
                                                                                                                                                                                                                                                                                                                                                                                        YSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGYELLKLDGIRGYCFDIDECSQRTHGCSDQMLCENLNGSYTCL--CPPGYALGLDNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTNGFD---LDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNP
                                                                                                                                                      CSHECINKAGTFECGCPLGYILNDDGRSCSPALVGCPPGTQRSADGCAPIECNPGYTLGS
                                                                                                                                                                                                                                 PDGFGCADIDECSQDYGNCSDICINLLGTHACACERGYELAKDKLSCLDVDECAGLLSGG
                                                                                                                                                                                                                                                                      EDGRSCODVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFL
                                                                         DDKCVDIDECQKQNGGCS - - HRCSNTEGSFKC -
                                                                                                             -----DINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNR-CM----CPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1394 13
1394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD29380E3162F68A CRC64;
                                                                           --- SCPPGYELDSDQKTCQDIDECDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat.
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                                                                                                                                                                                                                                 736
                                                                                                                                                                                                                                                                                                             676
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ð В Ş В

458

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560

TVNTVINFRGSSVIR-----LRIYVSQYPF KVNIHTKSRTGVILAFNEAIIEISVSKYPF

589 423 VPFSVDYNLDYVGQRHFRIVQERNIG----

Q9UH16; 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,

Q9UH16

PRELIMINARY;

PRT;

554

Ŗ

DJ162H14.1 (Fibulin 1) (Fragment).

Last sequence up Created)

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vo Catarrhini;

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ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQGIDECVTGIHNCSINETCFNIQGGFRCL
                                                           LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI
                                                                                                                EDGRSCQDVNECATENPCVQTCVNTYGSEICRCDDGYELEE-DGVHCSDMDECSF--SEF
                                                                                                                                                         VNSPGSFRCECKTGYYFDGISRMCVGVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS
                                                                                                                                                                                                                                                                                               QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                VDGRSCEGINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEGIDECALFTGGH
                                                                                                                                                                             ------QKNVPN------CGRGYHLNEEGTRCVGVDECAPPAEPCGKGHRC
                                                                                                                                                                                                                                              TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC
                                                                                                                                                                                                                                                                            QCKSGFIQD-ALGNCIGINECLSISAPCPIGHTCINTEGSYTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIISPIEVSRIVTHMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                               FE285184599A2982 CRC64;
                                                                                                                                                                                                                                                                                                                                                      .5; DB 4;
9.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IVQLVKPISGP----TVETI 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                        100;
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                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                    554;
                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                465
                                                                                                                                                                                      174
                                                                   290
                                                                                                                             231
                                                                                                                                                         406
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                                                                                                                            Matches
                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                        Interpro; IPRO0020; Anaphylatoxin.
Interpro; IPRO00561; EGF-like.
Interpro; IPRO00561; EGF-like.
Interpro; IPRO01881; EGF-like.
Interpro; IPRO01881; EGF-Like.
Interpro; IPRO01881; EGF-Ca.
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 5.
SMART; SM00179; EGF_CA; 4.
SMART; SM00179; EGF_Like; 6.
SMART; SM00001; EGF_Like; 6.
PROSITE; PS001177; ANAPHYLATOXIN_1; UNKNOWN_1.
PROSITE; PS01186; EGF_L; 4.
PROSITE; PS01186; EGF_CA; 8.
PROSITE; PS01187; EGF-Like domain; Glycoprotein; Hyd SEQUENCE 798 AA; 87205 MM; 3BF1EE9ED54D8BF9 CRC
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 268749; CAA92962.1; JOINED
EMBL; 268219; CAA92483.1; JOINED
EMBL; 268749; CAA92483.1; JOINED
EMBL; 268749; CAA92483.1; JOINED
HSSP; P16109; 1FSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lloyd C.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Latster N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; NemataRhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Wilkinson J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19, F56H11.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                018026; Q209
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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       240
                                    52
                                                                                                                            159;
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                                                                                                                                     Similarity
NAPRRMRDDPYSR---AGEYREASQANTEFGCPMGWLFQHGHCVDIDECATLMDDCLESQR
                                                       CRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRISRLVPHRHRANRIG
                                                                           RGP---YSNPYSTPYSGPYPAAAPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q20903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JAN-1996)
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                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                     23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases.
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                                                                                                                         49;
                                                                                                                   Score 574; DB 5;
Pred. No. 8.7e-50;
49; Mismatches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798
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                                                                                                                      172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                             Hydroxylation;
CRC64;
                                                                                                                                              Length
                                                                                                                   Indels
                                                                                                                   214;
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                                                                                                                 Gaps
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7.
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                             73
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RESULT 12
Q9UH16
ID Q9UH16
AC Q9UH1
AC Q9UH1
DT 01-MA
DT 01-DE
PELMAT
DT 01-MA
DT 01-DE
PELMAT
OC Mamma
OX HOMO
OC ELMAT
OC Mamma
OX NCBI\_
RP SEQUE
RA LLOYd
RI SUBMI
DR HSSP;
DR HSSP;
DR HSSP;
DR HSSP;
DR Inter
DR SMARTI
DR SMARTI
DR SMARTI
DR PROSI
DR PR

InterPro; InterPro; InterPro;

IPR000152; IPR000561; IPR001881;

Asx\_hydroxyl. EGF-like. EGF\_Ca.

Submitted (DEC-1999) to t EMBL; Z98047; CAB62995.1; HSSP; P35555; 1EMN.

SEQUENCE FROM N.A.

Lloyd D.

InterPro; IPR000020; Anaphylatoxin.

Query Match Best Local Simi Matches 114;

Similarity

Conservative

46;

Score 581.5; Pred. No. 9.7e 6; Mismatches

Pfam; PF01821; ANATO; 3.

Pfam; PF00008; EGF; 6.

SMART; SM00104; ANATO; 3.

SMART; SM00179; EGF\_CA; 4.

SMART; SM00001; EGF\_11ke; 5.

PROSITE; PS01177; ANAPHYLATOXIN\_1; 3

PROSITE; PS01178; ANAPHYLATOXIN\_2; 3

PROSITE; PS00101; ASX\_HYDROXYL; 4.

PROSITE; PS01186; EGF\_2; 3.

... ω

EGF-like domain; Glycoprotein; Hydroxylation. NON\_TER 1 1

554 AA;

59767 MW; 24.28;

В Š В QΥ В δÃ 밁 Ş 밁

> 407 175 347

308 120

266 13

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291 466

DPIRCEEPYLR 301

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RESULT 10
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Best Local S
Matches 151
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042182;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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Pfam; PF00008; EGF; ANATO; 2.

SMART; SM00104; ANATO; 2.

SMART; SM001079; EGF_CA; 5.

SMART; SM00001; EGF_Ike; 4.

PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.

PROSITE; PS01178; ANAPHYLATOXIN_2; 1.

PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; El
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01186; EGF_2; 3.

PROSITE; PS01187; EGF_CA; 6.

PROSITE; PS01187; EGF-11ke domain; Glycoprotein; Hydroxylation; Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; SEQUENCE 681 AA; 74459 MW; 175C966305A46699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Genes Evol. 0:0-0(1997)
EMBL; AF013751; AAB80944.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence of zebrafish fibulin-1 and heart and other embryonic organs.";
Dev. Genes Evol. 0.0-0/1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESP; P35555; IEMN.
ZFIN; ZDB-GENE-990415-73; fbln1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBLN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibulin-1 D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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      385
                                               584
                                                                                          333
                                                                                                                                  527
                                                                                                                                                                                                                      467
                                                                                                                                                                                                                                                                                                            408
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                                                                                                                                                                                                                                                               231
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                                                                                                                                                                                                                                                                                                                                                    174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P35555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                          FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPTQIC
: | || :| | :||| :| | : |
    IKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                     GRSVPADIFQMQATT----
                                                                                                                                                                                                                 HICSYRCHNTPGSFHCTCPASGYTLAANGRSCQDIDECLTGTHSCSESESCFNIQGGFRC
                                                                                                                                                                                                                                                                                                     ADDGRNCDDVNECES-SPCSQCCANVYGSYQSYCRRGYQLSDADGITCEDIDECALPTGG
                                                                                                                                                                                                                                                                                                                                                NEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCAAGFIQD-ALGSCIDINECVSVTALSRG-QMCFNTVGSFICQRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                             EFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSFDIIKRLDHGMIVGVVKQVRP
                                                                                                                              LS-FDCPANYRRSGDTRPRVDRADIIRCVKSCQHNDISCVLNP--ILSHSHTAISLPTFR
                                                                                                                                                                             IDPIRCEEPYLRISDN-----
                                                                                                                                                                                                                                                                                                                                                                                           INLYGSYRCECRTGFIFNSISRSCEDIDECR-NYPGRLCAHKCENILGSYKCSCTAGFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                   INTEGGYTCSCTDGYWL--LEGQCLDIDECRYGY----CQQLCANVPGSYSCTCNPGFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000020;
IPR000152;
IPR000561;
IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 05, (TrEMBLrel. 05, TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anaphylatoxin.
Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                     -RYPGAYYIFQIKSGNEGREFYMRQT---GPISATLVMTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 629.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VTCGRGYHLNAEGTRCVDIDECAGPDNSCD-GHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                         -RCM--CPAENPGCRDQPFTILYRDMDVVS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TZS1;
Q9TZS1;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000152; Asx_hydroxyl.
InterPro: IPR000561; EGF_like.
InterPro: IPR000561; EGF_like.
InterPro: IPR000881; EGF_Ca.
Pfam; PF00008; EGF; 6.
SMART; SM00179; EGF_CA; 5.
SMART; SM000179; EGF_Like; 4.
PROSITE; PS00010; ASX_HYDROXYL; 4.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01187; EGF_CA; 7.
Calclum-binding; EGF_CA; 7.
Calclum-binding; EGF_CA; 7.
Calclum-binding; EGF_CA; 7.
Calclum-binding; EGF_CA; 7.
SEQUENCE 589 AA; 63984 MW; 8EA3E8FCE0B97BE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterization of the C. ele
Matrix Biol. 17:635-646(1998).
EMBL; AF070477; AAC24035.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBLN1.
Caenorhabditis elegans.
Cukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; meloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CB1489 HIM-8;
MEDLINE-99120531; PubMed-9923656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barth J.L., Argraves K.M., Roark E.F., Little C.D., "Identification of chicken and C. elegans fibulin-1 characterization of the C. elegans fibulin-1 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P16109; 1FSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibulin-1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
156; Conserv
                                                                                                                            TIGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTK
                                                                                                                                                                                                                                                            FTLNE--
                                                                                                                                                                                                                                                                                                                                                                                           RNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CINGFDLDRQSGQCLD-IDECRIIPEACRGDMMCVNQNGGYLCIPRINPYIRGPYSNPYS
                                          GSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIH
                                                                                   GTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLR
                                                                                                                                                                         ATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF----SEFLCQHECVNQP
                                                                                                                                                                                                                    YEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNEC
                                                                                                                                                                                                                                                                                                     CVNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPG
                                                                                                                                                                                                                                                                                                                                                -------NVPGSYSCTCNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                      INTEGGYTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRSGFDLAPDGMACVDHIDECATLMDDCLESQRCLNTPGSFKCI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------RTLSCGTGYAMDSETERCRDVDECNLGSHDCGPLYQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPTQIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%;
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19,
-MCPAENPGC-RDQPFTILYRDMDVVSGRSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 592.5; DB 5;
Pred. No. 7.8e-52;
2; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                             -DGRSCQDVNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO00152; Asx_hydroxy1.
InterPro; IPRO00561; EGF-1ike.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO0186; EGF_Ca; 8.
SMART; SM00179; EGF_CA; 8.
SMART; SM00001; EGF_1ike; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4.
PROSITE; PS001186; EGF_Ca; 9.
Calcium-binding; EGF_Ca; 9.
Calcium-binding; EGF_Ch; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y3V7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wambutt R., Heubner D., Mewe Submitted (MAR-1999) to the EMBL; AL050095; CAB43267.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKFZP586A1519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 63.3 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cal Similarity
142; Conserv
      446
                                                                                 387
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                                                                                                 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
FECPPNYVQVSKTKC----ERTTCHDFLECQNSPARITHYQLNFQTGLLVPAHIFRIGPA
                                                                           TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R
                                                                                                                                                                                                                                                                                                                                      TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC 119
                                                                                                                                                                                                                                                                                                                                                                                                                              QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                                                                           EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC
                                                                                                                                                         ADGKRCEDVNECEAOR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC
                                                                                                                                                                                                                                    HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENTLGSYRCSCASGFLLA
                                                                                                                                                                                                                                                                             INTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN 174
                                                                                                                                                                                                                                                                                                                                                                                               RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-LECPENYRKSGDTVRLEKTDTIRCIKSCRPNDVNCVLDPVHTISHTVISLPTFREFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 703.5; DB 4;
34.5%; Pred. No. 3.5e-63;
                                                                                                                                                                                                                                                                                                                    ----QRNPLICARGYHASDDGTKCVDVNECETGVHRCGEGQVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mewes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gassenhuber J., Wiemann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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ID Q9HBQC5
DT Q01
DT Q1
DT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO00152; Asx_hydroxy1.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF-24.
Pfam; PF00008; EGF; 6.
SMARR; SM00181; EGF-CA; 9.
SMARR; SM00179; EGF-CA; 9.
SMARR; SM00010; EGF-11ke; 1.
PROSITE; PS001010; ASX_HYDROXYL; 3.
PROSITE; PS01186; EGF-2; 3.
PROSITE; PS01187; EGF-CA; 8.
EGF-11ke domain; Glycoprotein; Hydro SEQUENCE 495 AA; 54340 MW; C4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gu J.R., Wan D.F., Zhao
Qin W.X., Huang Y., Qiu
Yu J., Han L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9HBQ5 PRELIMINARY; PRT; 495 AA.
O9HBQ5:
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence up
O1-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 54.3 kba protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Novel Human cDNA clones with function of inhibiting cancer cell growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF217999; AAG17241.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P35555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                  VPGD----SMQAGHHRRQ
                                                                                                                                                                                                                                                  VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                     YPGAYYIFQIKSGNEGRE
                                                                                                                                                                       LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
                                                                                                                                                                                                                                                                         EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF
                                                                                                                                                                                                                                                                                                                                VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS
                                                                                                                                                                                                                                                                                                                                                    INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC--------
                                                                                                                                  DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSSA
                                                                                                                                                                                                                                                                                                                                                                                                           -----QKNVPN------CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDFALDVEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 674.5; DB 4;
Pred. No. 2.7e-60;
8; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou
Qian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydroxylation; Hypothetical protein.
C40434E6C82E3D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.F.,
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He L.P., Li H.N.,
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Yu Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO117; ANAPHYLATOXIN_1; 3.

PROSITE; PSO1178; ANAPHYLATOXIN_2; 3.

PROSITE; PSO1106; ASX, HYDROXYL; 5.

PROSITE; PSO1186; EGF_2; 5.

PROSITE; PSO1186; EGF_2; 5.

PROSITE; PSO1187; EGF_CA; 9.

Calcium-binding; EGF-like domain; Glycc SEQUENCE 1174 AA; 126460 MW; 8D628A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01821; ANATO; 2.
Pfam; PF00008; EGF; 6.
SMART; SM00104; ANATO; 3.
SMART; SM00181; EGF; 11.
SMART; SM00179; EGF_CA; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99K58;
Q99K58;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EMBL; BC005443; AAH05443.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                 234
                                                                                                                                                                                                                                            120 INTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN
                                                                                                                                                                                                                                                                                                                                                                                 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
145; Conserv
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IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT
                                                     TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R 1043
                                                                                           QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP
                                                                                                                                      ADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC
                                                                                                                                                             EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC
                                                                                                                                                                                                                   YNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSCAAGFLLA
                                                                                                                                                                                                                                                                                                                       TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC
                                                                                                                                                                                                                                                                                                                                                                                                       QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
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                                                                                                                                                                                                                                                                                                                                                                               RCMDGF-LQDPEGNCVDINECTSLLEPCRSGFSCINTVGSYTC-----
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(TrembLrel. 17, Last seq
(TrembLrel. 21, Last ann
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Rodentia;
                                                                                                                                                                                                                                                                                                  -----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEGQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 731.5; DB 11;
Pred. No. 1.1e-65;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Hydroxylation; 8D628AC710FBA6B8 CRC64;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
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Best Local S
Matches 160
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073774;
01-AUG-1998
01-AUG-1998
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                  DPIRCEEPYLRISDN----
                                                                                                                                                       EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF
                                                                                               LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI
                                                                                                                                    SDGRSCEDLNECES-SPCSQECANYYGSYQCYCRRGFQLSDIDGISCEDIDECALPTGGH
                                                                                                                                                                                                                                                                                                                                                                            QCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-QRISP------
                                                                                                                                                                                                                                                                                                                                                                                                                      QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                            ICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCSFNETCFNIQGGFRCL
                                                                                                                                                                                                                   INGPGNYRCECKSGYSFDVISRTCIDINECRRYPGRLCAHKCENTPGSYYCTCTMGFKLS
                                                                                                                                                                                                                                                        INTEGGYTCSCTDGYW---LLEGQCLDIDECRY---GYCQQLCANVPGSYSCTCNPGFTLN 174
                                                                                                                                                                                                                                                                                                                       TPYSGPYPAAAPPLSAPNYPTISRPLICREGYQMDE-SNQCVDVDECATDSHQCNPTQIC
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Gremburel.
Gremburel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                    -----SCGRGYHLNEDGTRCVDVDECSSSDQPCGEGHVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%;
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64;

Indels

78;

Gaps

21;

60 340

374 119

-CPAENPGC-RDQPFTILYRDMDVVSGRSV--

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В
                                                                                    Pfam; PF00008; EGF; 6.

SMART; SM00104; AMATO; 3.

SMART; SM00104; EGF_CA; 8.

SMART; SM00101; EGF_Like; 1.

PROSITE; PS01177; ANAPHYLATOXIN_2; 2.

PROSITE; PS01178; ANAPHYLATOXIN_2; 2.

PROSITE; PS01118; ANAPHYLATOXIN_2; 2.

PROSITE; PS011186; EGF_C; 3.

PROSITE; PS011187; EGF_CA; 8.

PROSITE; PS011187; EGF_CA; 8.

PROSITE; PS011187; EGF_CA; 8.

PROSITE; PS011187; EGF_CA; 8.

PROSITE; PS011187; EGF_CA; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of chicken and C. elegans fibulin-1 characterization of the C. elegans fibulin-1 gene."; Matrix Biol. 17:635-646(1998).
EMBL; APOS1399; AACO5387.1; -.
HSSP; p00742: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBLNI.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Neoqnathae; Galliformes; Phasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99120531; PubMed-9923656;
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDCPPNYVRVSETKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRIGPA 1099
                                                                                                                                                                                                                                                                                                                                                                                   EGF_Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07,
19,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Score 713; DB 13;
Pred. No. 4.8e-64;
4; Mismatches 154;
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                                                                                              Hydroxylation;
CRC64;
                                            Length
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homologs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phasianinae;
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                                                                                                                             Query Match
Best Local S
Matches 158
                                                                                                                                                                                   Interpro; IPR000020; Asaphylatoxin.
Interpro; IPR000050; Asaphydroxyl.
Interpro; IPR000561; EGF-1ike.
Interpro; IPR000561; EGF-2ike.
Interpro; IPR000561; EGF-Ca.
Pfam; PF01021; ANATO; 3.
Pfam; PF01021; ANATO; 3.
Pfam; PF01071; ANAPHYLATOXIN_1; UPR0SITE; PS01178; ANAPHYLATOXIL, UNKN PROSITE; PS01178; ANAPHYLATOXIL, UNKNOWN_3.
PROSITE; PS01187; EGF_CA; UNKNOWN_3.
PROSITE; PS01187; EGF_CA; UNKNOWN_8.
SEQUENCE 685 AA; 75283 MW; EF0D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q922K8;
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2001) to the EMBL; BC007140; AAH07140.1; MGD; MGI:95487; Fbln1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Strausberg R.;
Submitted (APR-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-JUN-2002 (TremBLrel.
Similar to fibulin 1.
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                                                                                                                                            Similarity
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                                                                               QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
                                                            OCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC
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                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                      ANAPHYLATOXIN_1; UNKNOWN_3.
ANAPHYLATOXIN_2; 3.
ASX_HYDROXYL; UNKNOWN_4.
EGF_2; UNKNOWN_8.
EGF_CA; UNKNOWN_8.
EGF_CA; UNKNOWN_8.
                                                                                                                                            30.8%;
36.5%;
   -OKNVPN--
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19,
21,
                                                                                                                             64;
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Last sequence update)
Last annotation updat
                                                                                                                           Score 741.5; DB 11; Length Pred. No. 5.7e-67; 14; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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-CGRGYHLNEEGTRCVDVDECSPPAEPCGKGHHC
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                                                                                                                           59;
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                                                                                                                           Gaps
375
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Best Local :
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01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB-2002) to the EME
EMBL; BC022497; AAH22497.1; -.
SEQUENCE 683 AA; 74423 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TBH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8TBH8
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                                                                                                                                                                                                                                                                                                                                                                                    155;
                                                                                                                                                                                                                                                                                      61
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                                                         TPYSGPYPAAAPPLSAPNYPTISRPLICREGYQM-DESNQCVDVDECATDSHQCNPTQIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH
-AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSSA
                            DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTR
                                                                                                                                                                                                                                                                                                                    QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPGDSMQLAITAGNEEGFFTTRKVSHHSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-FECPENYRRSADTRCERLPCHENQECPRLPLRITYYHLSFPTNIQVPAVVFRMGPSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF
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2 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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21,
21,
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 735.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2665A3961B6403B4 CRC64;
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                                                       Query Match
Best Local Sir
Matches 220;
                                                                                                                                                 MGD; MGC:189109; Efemp2.

R InterPro; IPR000561; EGF-Like.

R InterPro; IPR000561; EGF-Like.

R InterPro; IPR001891; EGF-Like.

R InterPro; IPR001891; Thrmbomoduln.

Pfam; PF00008; EGF; 4.

R Pfam; PF00009; THRMBOMODULN.

R SMART; SM00179; EGF_CA; 4.

R SMART; SM00001; EGF_Like; 2.

R SMART; SM00001; EGF_Like; 2.

R PROSITE; PS001186; EGF_2; 4.

R PROSITE; PS01186; EGF_CA; 6.

R PROSITE; PS01187; EGF_CA; 6.
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01-JUN-2002 (Tr
EGF-containing
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01-ост-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITINE=20435063; PubMed=10982184;
Katsanis N., Venable S., Smith J.R., Lupski J.R.;
"Isolation of a paralog of the Doyne honeycomb retinal from the multiple retinopathy critical region on 11q13. Hum. Genet. 106:56-72(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-20435063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                               Similarity
QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
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                                                       Conservative
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Last annotation update)
extracellular matrix protein
                                              Score 1273.5;
Pred. No. 1.6e
65; Mismatches
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  Matches
                           Query Match
Best Local
                                                                                                                     InterPro; IPRO00152; Asx_hydroxy1.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001481; Thrmbomoduln.
Pfam; PF00008; EGF; 3.
PRINTS; PR00907; THRMBOMODULN.
SMART; SM00181; EGF; 5.
SMARR; SM00181; EGF_CA; 6.
SMARR; SM0019; EGF_Like; 2.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 5.
PROSITE; PS01187; EGF_CA; 5.
PROSITE; PS01187; EGF_CA; 5.
PROSITE; PS01187; EGF_CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seibold S., Marx M.;
"Cloning of a new fibulin-like gene.";
"Cloning of Jan-199) to the EMBL/GenBank/DDBJ
EMBL; AF124486; AAG45245.1;
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H3D5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                  ); PS00010; ASX_HYDROXYL;

); PS01186; EGF_2; 4.

); PS01187; EGF_CA; 5.

); PS01187; EGF_CA; 5.

Edomain; Glycoprotein; H;

Ed43 AA; 49535 MW; D;
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Primates;
                     52.1%;
  67;
Score 1253.5;
Pred. No. 1.8e
67; Mismatches
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Catarrhini; Hominidae
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                                                                                                       Hydroxylation; Matrix protein. D91784BF36A8A060 CRC64;
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                           5; DB 4;
..8e-119;
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  122;
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  17;
Gaps
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Result
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Maximum DB
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Perfect score:
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SP_Archea:*

Sp_bacteris

Sp_fungi:*

Sp_bundi:*

Sp_fungi:*

Sp_fungi:*

Sp_fungi:*

Sp_fungi:*

Sp_fungi:*

Sp_punamma

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10: Sp_p

11: Sp_y

12: Sp_y

13: Sp

14: Sp

15: Sp

16: Sp_Sp

16: Sp_Sp

17:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
1276.5
1273.5
1253.5
741.5
735.5
7315.5
731.5
703.5
629.5
6292.5
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length: 2000000000
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Listing
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2407
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sp_bacteria:*
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sp_bacteriap:*
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sp_unclassified:*
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first 45 summaries
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09H3M6
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08TBH8
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Compugen Ltd
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Q9jm06 mus musculu
Q9h3d5 homo sapien
Q922k8 mus musculu
Q8tbh8 homo sapien
Q99k58 mus musculu
Q73774 gallus gall
Q9y3v7 homo sapien
Q9hbq5 homo sapien
Q9hbq5 homo sapien
Q42182 brachydanio
Q9tzsl caenorhabdi
Q9uh16 homo sapien
Q9h16 homo sapien
Q9vs89
Q96sc3
Q8td95
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drosophila
homo sapien
homo sapien
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Q9eqc6 mus			_	460.5	•
Q25678 podocoryne	o		N	462.5	
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075441 homo	0		5	468.5	
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Q9tvq2 caenorhabd1	5 Q9TVQ2		5	469.5	
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Q9h7k2 homo	4 Q9H7K2	.382 4		474	
	4 Q9NS15	256 4	9.7	474	
	4 Q96нв9	746 4	9.7	474	
Q9np01 homo	4 Q9NP01		0.0	480.5	
035806 rattus norv	11 035806		0.0	482.5	
-	5 Q9V4B8		0.1	483.5	
Q28019 bos taurus			0.1	484.5	
Q9blj1 ciona intes	5 Q9BLJ1		0.4	491.5	
Q9wuh9 rattus			1.0	506.5	
P87363 gallus			1.1	507.5	
Q8rlu8 mus			1.1	508	
Q96jp8 homo	4 Q96JP8	809 4	.ω	511.5	
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Q96k89 homo	4 Q96K89	741 4	1.5	517.5	
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## ALIGNMENTS

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                                                                                                                                             Query Match
Best Local Similarity
Matches 220; Conserv
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"Human mutant p53 binding protein (MBP1).";
"Human mutant p53 binding protein (MBP1).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AB030655; BAA92880.1;
"InterPro; IPR000152; BAX_hydroxyl.
InterPro; IPR000152; GST_like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        096TF5;
01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Tanka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant p53 binding protein MBP1.
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PROSITE; PS01186; EGF_2; UNKNOWN_4.
PROSITE; PS01187; EGF_CA; UNKNOWN_6.
SEQUENCE 443 AA; 49421 MW; 9CE175F4F38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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38
                                   ECTDGYEWDPDSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVINDLHG----
                                                                                                                                                 53.0%; ilarity 52.0%; Conservative 6
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                                                                                                                                                 ; Score 1276.5; DB; Pred. No. 8e-122; 67; Mismatches 11
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126; Conservative
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                                                                                  SYMCSCHKGYTRTPDHKHCRDIDECOOGNLCVNGQCKNTEGSFRCTCGQGYQLSAAKDQC
                         -TCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQH-ECV
                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
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Pred. No. 1e-33;
1; Mismatches 126
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Db	Qy	DЬ	Qy .	DЬ	Qy	
964 ELLSG 968	329 DVVSG 333	VCDSHG:	291 -DPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328	852 NTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSFHCVCQQGFSIS 909	239 NQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290	
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Search completed: July 3, 2003, 18:23:14
Job time: 10.6843 secs

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RESULT 15
LTBS_HUMAN
ID LTBS_HA
AC P22064
DT 01-AUG
DT 15-JUN
DE Latent
DE (Trans
DE 1).
GN LTBP1.
OS Homo s
OC Eukary,
OC Mammal
OX NCBLT
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA Kanzak
RA Miyazo
RT "TGF-b
RT Of TGF
                                                                                                                 BS_HUMAN

LTBS_HUMAN

LTBS_HUMAN

C P22064;

T 01-AUG-1991 (Rel. 19, Created)

T 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-MU-2002 (Rel. 41, Last annotation update)

DE Latent transforming growth factor beta binding pro-

"Transforming growth factor beta-1 binding protein
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Best Local
     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Fibroblast, and Platelet;
MEDLINE-90275601; PubMed-2350783;
Kanzaki T., Olofsson A., Moren A., Wernstedt C.,
Miyazono K., Claesson-Welsh L., Heldin C.-H.;
"TGF-beta 1 binding protein: a component of the ]
of TGF-beta 1 with multiple repeat sequences.";
                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
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Catarrhini;
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i; Hominidae;
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    InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001881; EGF-Ca.
InterPro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 15.
Pfam; PF00008; TB; 4.
SMART; SM00179; EGF-CA; 13.
SMART; SM00101; EGF_1ike; 4.
PROSITE; PS00010; ASX_HYDROXYL; 13.
PROSITE; PS01186; EGF_2; 11.
PROSITE; PS01186; EGF_CA; 15.
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or send an email :
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; P00750; ITPG.
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HGNC:6714; LTBP1.
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                                                                                                              959
1017
1097
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                                                                                                                                                                                                                                                                                                                                                binding;
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; EGF_2; 11.
; EGF_CA; 15.
  1394
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EGF-LIKE
REPEAT C.
EGF-LIKE
REPEAT C.
EGF-LIKE
REPEAT B.
SIMILA
BY SIMILA
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Y SIMILARITY.
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Signal;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial 1 61:1051-1061(1990).

SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE "TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

ALTERNATIVE PRODUCTS: 2 isoforms; a short form (shown here) and a long form (AC Q14766); are produced by alternative splicing. PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES.

SIMILARITY: CONTAINS 15 blocked.

SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS. (See http://www.isb-sib.ch/announce/

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RESULT 14
FBLI_CAEEL STANDARD; PRT; 712 AA.
ID FBLI_CAEEL STANDARD; PRT; 712 AA.
C 077469; 077474; Q9SNZ3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-DCT-2002 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibulin-1 precursor.
FBLN1 OR F56HI1.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rha
OC Enhabditidae; Peloderinae; Caenorhabditis.
OX NCB1 TayID6230.
       EMBL;
EMBL;
EMBL;
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EMBL;
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MEDLINE-99120531; PubMed-9923656;

Barth J.L., Argraves K.M., Roark E.F., Little C.D., i

"Identification of chicken and C. elegans fibulin-1 |

characterization of the C. elegans fibulin-1 gene.";

matrix Biol. 17:635-646(1998).
                                                                                                                                                          or send
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                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
  C; AF051403; AAC28323.1; -...
AF051401; AAC28324.1; -...
AF051401; AAC28321.1; -...
Z68219; CAC35826.1; -...
Z68219; CAC35826.1; -...
Z68219; CAC35827.1; -...
Z68749; CAC35827.1; -...
Z68749; CAC35817.1; JOINED
Z68749; CAC35817.1; JOINED
Z68749; CAC35817.1; JOINED
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      PROSITE; PS00010; /
PROSITE; PS01177; /
PROSITE; PS01186; I
PROSITE; PS01187; I
Signal; Glycoprote;
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InterPro; IPR000152; Ass
InterPro; IPR000561; EGI
InterPro; IPR001881; EGI
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Pfam; PF00008; EGF; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z68219; CAC35818.1; JC WormPep; F56H11.1a; CE26701. WormPep; F56H11.1b; CE26702. HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium-binding;
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                                                      7; ANAPHYLATOXIN_1;
5; EGF 7: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF_2; 5.
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EGF-like.
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ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 3.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5.
EGF-LIKE 6.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 8.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 8.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
EGF-LIKE 9.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
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(POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).

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RARE RARE RAPER RA

      Pfam;
      PF00008;
      EGF;
      6.

      Pfam;
      PF00008;
      EGF;
      6.

      Pfam;
      PF00018;
      ANATO;
      3.

      SMART;
      SM001019;
      EGF_Ca;
      7.

      SMART;
      SM00001;
      EGF_1 ke;
      7.

      SMART;
      SM00001;
      EGF_1;
      FA

      PROSITE;
      PS00102;
      EGF_1;
      FA

      PROSITE;
      PS0117;
      ANAPHYLATC
      PROSITE;
      PS01118;
      EGF_2;
      3.

      PROSITE;
      PS011187;
      EGF_CA;
      8
      SIGNAL
      1
      29
      CHAIN
      703

      PROSITE;
      PS01187;
      EGF_CA;
      8
      SIGNAL
      1
      29
      CHAIN
      703
      CHAIN
      703
      CHAIN
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      CHAIN
      703
      CHAIN
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      111
      DOMAIN
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      215
      DOMAIN
      176
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      DOMAIN
      262
      307
      307

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EMBL; X53742; CAA37772.1; -
EMBL; X53743; CAA37772.1; -
EMBL; U01244; AAB17099.1; -
EMBL; Z95331; CAB62960.1; -
PIR; A36346; A36346.
PIR; B36346; B36346.
PIR; B36346; B36346.
PIR; C36346; C36346.
PIR; C36346; C36346.
PIR; C36346; C36346.
PIR; C36346; C36346.
RSSP, P35555; IEMN.
Genew; HGNC:3600; FBLN1.
MIM; 135820; -
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000020; A InterPro; IPR000152; A InterPro; IPR000561; E InterPro; IPR001881; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE: OF
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Submitted
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Argraves S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS A; B MEDLINE-91100426; PubMed-2269669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89354537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeated domain structure.";
J. Cell Biol. 111:3155-3164(1990)
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SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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'ires a license a
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                                                                                                                                                                                         ASX_HYDROXYL; 4.
BGF_1; FALSE_NEG.
RANAPHYLATOXIN_1;
ANAPHYLATOXIN_2;
BGF_2;
BGF_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-2527614;
                                                                                                                                                                             splicing;
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EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anaphylatoxin.
                                                                                                                                                                                                                                                                                                                                                                                                     EGF_Ca.
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                                                                                                                                                      ring; Glycoprotein; Calcium-binding.
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   FIBULIN-1.
ANAPHYLATOXIN-LIKE 1
ANAPHYLATOXIN-LIKE 2
ANAPHYLATOXIN-LIKE 3
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-
EGF-LIKE 3, CALCIUM-
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     CALCIUM-BINDING CALCIUM-BINDING
                                                                                                                                                                         Extracellular matrix;
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(POTENTIAL).
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Best Local S
Matches 159
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CONFLICT
SEQUENCE
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               INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN
                                                     -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC
                                                                     TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC
                                                                                                                                QCKSGFIQD
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41
703 AA;
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                                                                                                                                                                                                                             28.8%;
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Pred. No. 7.6e.
65; Mismatches
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EGF-LIKE 5, CALL
EGF-LIKE 7, CALL
EGF-LIKE 8, CALL
EGF-LIKE 9, CALL
EGF-LIKE 9, CALL
EGF-LIKE 9, CALL
EGF-LIKE 17, CALL
EGGF-LIKE 17, CALL
EGGF-LI
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MISSING (
                                                                                                                                                                                                                                                                                VAKLFIFVSAEL (IN ISOFORM C -> S (IN REF. 4).
HR -> SH (IN REF. 4).
EFD88465BA2D3A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                         NVVNVRIFVSEYWF -> RCERLPCHENRECSKLPLRITYY
HLSFPTNIQAPAVVFRMGPSSAVPGDSMQLAITGGNEEGFF
TTRKVSPHSGYVALTKPVPEPRDLLLTVKMDLSRHGTVSSF
                                                                                                                                                                                                                                                                                                                                                                                                               ISOFORM B)
LQQEKTDTVRCIKSCRPNDVTCVFDPVHTISHTVISLPTFR
EFTRPEEIFIRAITPPHPASQANIIFDITECNLRDSFDII
KRYMDGMTVGVVRQVRPIVGPFHAVLKLEMNYVVGGVVSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQQEKTDTVRCIKSCRPNDVTCVFDPVHTISHTVI ->
SKKGRQNTPAGSSKEDCRVLPWKQGLEDTHLDA (IN
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CALCIUM-BINDING
CALCIUM-BINDING
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CALCIUM-BINDING
CALCIUM-BINDING
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.6e-46;
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149;

Indels

Gaps

334 60

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Length

ISOFORM C).

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(POTENTIAL).
(POTENTIAL).

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Pfam; PF00008; EGF; 7.

Pfam; PF01821; ANATO; 2.

SMART; SM00104; ANATO; 3.

SMART; SM001079; EGF_CA; 9.

SMART; SM00001; EGF_L1ke; 1.

SMART; SM00001; ASX_HYDROXYL; 5.

PROSITE; PS01177; ANAPHYLATOXIN_1; 3

PROSITE; PS01178; ANAPHYLATOXIN_2; 3

PROSITE; PS01187; EGF_1; PALSE_NEG.

PROSITE; PS01187; EGF_CA; 9.
                       DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
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SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX. COMPONENT
BASEMENT MEMBRANES AND OTHER CONNECTIVE TISSUES.
TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND
SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institutions as long as its content is in no way non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
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                         Extracellular matrix;
                    SUBDOMAIN NA (CYS-RICH).
SUBDOMAIN NA (CYS-FREE).
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
EGF-LIKE 4, CALCIUM-BINDING.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 9, CALCIUM-BINDING.
EGF-LIKE 10, CALCI
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                                                                                                                                                                                                                                                                                                                 3, CALCIUM-BINDING.
1, CALCIUM-BINDING.
5, CALCIUM-BINDING.
6, CALCIUM-BINDING.
7, CALCIUM-BINDING.
8, CALCIUM-BINDING.
10, CALCIUM-BINDING.
10, CALCIUM-BINDING.
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                                                                                                RESULT 13
FBL1_HUMAN STANDARD; PRT;
ID FBL1_HUMAN STANDARD; PRT;
AC P23142; P23143; P23144; P37888; Q9
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequenc
DT 15-JUN-2002 (Rel. 41, Last annotat
DE Fibulin-1 precursor:
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                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                1110 PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDFALDVEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                                                                                                                                                                                                   FECPPNYVQVSKTKC.
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                                                      Chordata;
Primates;
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                                                                                                                                    sequence update) annotation updat
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BY SIM
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Pred. No. 3.4e
58; Mismatches
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                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                     update)
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.4e-46;
les 152;
                                                      Hominidae;
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                                                                       Euteleostomi;
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292

935 233 994 174

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InterPro; IPRO00020; Anaphylatoxin.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00151; EGF-11ke.
InterPro; IPRO01881; EGF_CA.
Pfam; PF00008; EGF; 6.
Pfam; PF01821; ANATO; 3.
SMART; SM00104; ANATO; 3.
SMART; SM00104; ANATO; 3.
SMART; SM001079; EGF_CA; 7.
SMART; SM00101; EGF_11ke; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4.
PROSITE; PS001010; ASX_HYDROXYL; 4.
PROSITE; PS00110; ASX_HYDROXYL; 4.
PROSITE; PS00117; ANAPHYLATOXIN_1; 3.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01186; EGF_CA; 8.
PROSITE; PS01187; EGF_CA; 8.
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X70853;
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EGF-like dom
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      license agreement (See http://www.isb-sib.ch/announce/
license@isb-sib.ch).
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ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2.
CALCIUM-BINDING ()
EGF-LIKE 3.
CALCIUM-BINDING ()
EGF-LIKE 4.
CALCIUM-BINDING ()
EGF-LIKE 5.
CALCIUM-BINDING ()
EGF-LIKE 7.
CALCIUM-BINDING ()
EGF-LIKE 8.
CALCIUM-BINDING ()
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EGF-LIKE 9.
CALCIUM-BINDING ()
EGF-LIKE 9.
EGF-LI
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Best Local S
Matches 160
                                               TISSUE=Fibroblast;
MEDLINE=95104855; P
Zhang R.-Z., Pan T.
Chu M.-L.;
                                                                                    SEQUENCE
TISSUE-Fi
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CARBOHYD
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VARSPLIC
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p98095;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Fibulin-2 precursor.
  of the gene on human and r
Genomics 22:425-430(1994)
-!- FUNCTION: ITS BINDING
                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                    "Fibulin-2 (FBLN2): human
                                                                                                           NCBI_TaxID=9606;
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50; Conservative
                                                                                                FROM
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                                                         PubMed=7806230;
T.-C., Zhang Z.-Y.,
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N-LINKED (GLCNAC. . .) (POTENTIAL).

FROEKIDITYPACIKSCRPNDEACVRDPVHTVSHTVISLPTER
EFFRREEIIFLRAVTPLYPANQADITIFDITENLROSFDII
KRYEDGMTYGVVYQVEPIVGFPYAVKLEMNYVLGGVVSHR
KYYENGMTYGVVGVVERIVGFPYAVKLEMNYVLGGVVSHR
NVVNVHIFVSEYWF -> RCARLPCHENQECPRLPLRITYY
HLSFPTNIOVPAVVFRMGPSSAVPGDSMOLAITAGNEEGFF
TTRKVSHHSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSSF
VAKLFIFVSAEL (IN ISOFORM D).

MW; FD3F06469A4BAE2B CRC64;
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   FIBRONECTIN AND
                                                                                                                                 Craniata; Vo
Catarrhini;
                         sequence, mR chromosomes.
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i; Hominidae;
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   OTHER LIGANDS
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                                    mapping
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SMART; SM00179; EGF_CA; 9.

SMART; SM00001; EGF_like; 2.

PROSITE; PS00010; ASX_HYDROXYL; 5.

PROSITE; PS01179; ANAPHYLATOXIN_1; 3.

PROSITE; PS01178; ANAPHYLATOXIN_2; 3.

PROSITE; PS01186; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01187; EGF_CA; 10.

Signal; Glycoprotein; Extracellular r
Calcium-binding; Alternative splicing
    DISULFID
CARBOHYD
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; SM00104;
        ; ANATO; 2.
4; ANATO; 3.
9; EGF_CA; 9.
1; EGF_like; 2.
      Extracellular matrix; rnative splicing; Repe
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BY
SUBDOMAIN NA (CYS-RI
SUBDOMAIN NA (CYS-RI
SUBDOMAIN NA (CYS-RI
SUBDOMAIN NB (CYS-RE
ANAPHYLATOXIN-LIKE 1
ANAPHYLATOXIN-LIKE 2
ANAPHYLATOXIN-LIKE 1
ANAPHYLAT
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Repeat.
  LCNAC...
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s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for con
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ches 145; Conserv
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                                                       IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT
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EDCPPNYVRVSQTKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRIGPA
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PAFAGDTISLTITKGNEEGYFVTRRLNAYTGVVSLQRSVLEPRDFALDVEM
               TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R
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8 MW; 87DB2A10A8FDC45F C
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Pred. No. 2.6e
9; Mismatches
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FBLI_MOUSE STANDARI
Q08879; Q08878;
01-OCT-1994 (Rel. 30, 0
01-OCT-1994 (Rel. 30, 1
15-JUN-2002 (Rel. 41, 1
MEDLINE-93358897;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                              NCBI_TaxID=10090;
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Rodentia;
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Basement-membrane protein
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Pred. No. 1.3e-51;
2; Mismatches 150;
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P37889; Q9WUI2;
P37889; Q9WUI2;
O1-OCT-1994 (Re)
O1-OCT-1994 (Re)
15-JUN-2002 (Re)
                     HSSP; P00736; 1APQ.
MGD; MGI:95488; Fbln2.
InterPro; IPR0001020; Anaphylatoxin
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
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L AF135241;
L AF135243;
L AF1352443;
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40; AAD34456.1
141; AAD34456.1
142; AAD34456.1
243; AAD34456.1
244; AAD34456.1
245; AAD34456.1
246; AAD34456.1
247; AAD34456.1
248; AAD34456.1
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250; AAD34456.1
251; AAD34456.1
252; AAD34456.2
251; AAD34456.1
252; AAD34456.1
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AAD34456

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EUI. J. BIOCHEM. 263:471-477(1999).

-I FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER I CALCIUM DEPENDENT.

-I SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.

-I SUBCELLULAR LOCATION: Extracellular matrix.

-I ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown least).

-I FUNCTION: EXTRACTIVE SPOINT OF BOTH BASEMENT MEMBRICONNECTIVE TISSUES.

-I SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

-I SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 263:471-477(1999).

Eur. J. Biochem. 263:471-477 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94064787; PubMed-8245130; Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.; "Structure and expression of fibulin-2, a novel extracellular matrix protein with multiple EGF-like repeats and consensus motifs for calcium binding.";
J. Cell Biol. 123:1269-1277(1993).
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TISSUE-Fibroblast;
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mouse fibulin-2 gene.
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1 (Rel. 30,
2 (Rel. 41,
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7686; PubMed=10406956;
Sicot F.-X., Gotta S., Chu M.-L.
in-2 gene. Complete exon-intron c
CAA53040
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tions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                           203;
                                                                                                                                                                                                                                                                                               28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E; PS00022;
E; PS01186;
E; PS01187;
; EGF-like d
e mutation;
                                                                                                                                                                                                                                                                                                                                                     Similarity
                               QTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYI
                                                                                                                                                                                                                     PISATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                                                                                                                                          RIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQCPPGY
                                                                                                                                                                                                                                                   TQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFVIRRNPADPQ
                                                                                                                                                                                                                                                                                            QCTDGYEMDPVRQQCKDIDECDIVPDACKGGMKCVNHYGGYLCLPKTAQIIVNNEQPQQE
                                                                                                                                                                                                                                                                                                                  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVY----RGPYSN
                                                                                                                    QQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQ
                                                                                                                                                               QKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDASNQCA
                                                                                                                                                                                    WILLEGOCLDIDECRY-GYCOQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCV
                                                                                                                                                                                                                                                                                                                                                                                    493
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_1; F
EGF_2; 4
EGF_CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345
                                                                                                                                                                                                                                                                                                                                                                                    54640
                                                                                                                                                                                                                                                                                                                                                    45.4%;
43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                    X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                         STPYSGPYPAA----APPL
                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-CONTAINING FIBULIN-LIKE EXMATRIX PROTEIN 1.

EGF-LIKE 1, DYEFREBRY.

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 5, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()

EGF-LIKE 7, CALCIUM-BINDING ()

EGF-LIKE 8, CALCIUM-BINDING ()

EGF-LIKE 8, CALCIUM-BINDING ()

EGF-LIKE 9, CALCIUM-BINDING ()

EGF-LIKE 1, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 1, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 4, CALCIUM-B
                                                                                                                                                                                                                                                                                                                                                 Score 1093.5; DB 1; Length Pred. No. 1.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_009512.

R -> W (IN MVLT).

/FTId=VAR_009513.

128CA5ED140DF414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                         152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                    ( ) (POTENTIAL).
( 2).
( 3).
( 4).
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    147
                                                      373
                                                                                                313
                                                                                                                     325
                                                                                                                                           253
                                                                                                                                                                265
                                                                                                                                                                                      193
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                                                                                                                                                                                                                                                                                                                    57
                                                                           383
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FBL1_CHICK
ID FBL1_CHICK
AC 073775;
   밁
                                                                                                                                                                                                                                                                                Pfam; PF00008; EGF; 6.
Pfam; PF01821; ANATO; 2.
SMART; SM00104; ANATO; 3.
SMART; SM00179; EGF_CA; 8.
SMART; SM00001; EGF_like; 1
                                                              Caicium-binding.
SIGNAL 1
CHAIN 26
DOMAIN 33
DOMAIN 110
DOMAIN 117
DOMAIN 217
DOMAIN 217
DOMAIN 263
DOMAIN 309
DOMAIN 309
DOMAIN 309
DOMAIN 402
DOMAIN 402
DOMAIN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
Fibulin-1 precursor.
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                      DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                  InterPro;
Pfam; PFO
Pfam; PFO
                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                       PROSITE; PS00010; ASX_HYDROXYL; 5.
PROSITE; PS01177; ANRPHYLATOXYN 2.
PROSITE; PS01178; ANRPHYLATOXYN 2.
PROSITE; PS00022; EGF_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF051400; AACO: HSSP; P00742; 1HCG. InterPro; IPR000020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-99120531; PubMed-9923656;
                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444
                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                   PS01186;
PS01187;
                                                                                                                                                                                                                                                                                                                                       IPR001881;
                                                                                                                                                                                                                                                                                                                                                  IPR000152;
IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40,
(Rel. 40,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           AAC05388.1;
                                                                                                                                                                                                                   EGF_1;
EGF_2;
EGF_CA;
 Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                     Anaphylatoxin.
                                                                                                                                                                                                                                                                                                                                      EGF_Ca
                                                                                                                                                                                                         Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last
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                                                                                                                                                                                    POTENTIAL
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PVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF
493
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"Identification of chicken and C. elegans fibulin-1
characterization of the C. elegans fibulin-1 gene."
Matrix Biol. 17:635-646(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Secreted; extracellular
-1- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOM
-1- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for confided and this statement is not removed.
ANAPHYLATOXIN-LIKE I
ANAPHYLATOXIN-LIKE I
EGF-LIKE 1. CALCIUM
EGF-LIKE 3. CALCIUM
EGF-LIKE 4. CALCIUM
EGF-LIKE 5. CALCIUM
EGF-LIKE 5. CALCIUM
EGF-LIKE 6. CALCIUM
EGF-LIKE 7. CALCIUM
EGF-LIKE 8. CALCIUM
EGF-LIKE 9. CALCIUM
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; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix;
                                                                                                     CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
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CALCIUM-BINDING
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CALCIUM-BINDING
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CALCIUM-BINDING
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                                                                                                                                                                                                                                                                                                                                                 \omega \sim \Gamma
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homologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
idae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like
                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                             (POTENTIAL)
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain;
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RESULT 8
FBL3_HUMAN
ID FBL3_HUMAN STAN
AC Q12805;
DT 16-OCT-2001 (Rel. 4
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Best Local
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DOMAIN
DISULFID
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
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                                                                                                                                                       376
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                                                                                                                                                                                                                                                           328
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                                                                                                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                           268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                        CRDQPFTILYRDMDVVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPI
                                                                                                                                                                                                                                                                       DDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPG
:|:||||||| | ; |:| | ||:| | ;:||: |:||:|| |
                                                                                                                                                                                                                                                                                                                      RIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQVCINLRGSFTCHCLPGYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00010;
PS00022;
PS01186;
PS01187;
                                                                                                                                                     SATLYMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF
                                                                                                                                                                                       CRDVPQSIVYKYMNIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYLRQTSPV
                                                                                                                                                                                                                                                                                                                                                                                        LEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPYS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                                                                                                      SAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLTIIVGPFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPAAEASSGAATGTIAARSMATSGVIPGGGFIASATAVAGPEVQTGRNNFVIRRNPADPQ
                                                                                                                                                                                                                                                       -RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPQNPCQDPYVLTSENRCVCPVSNTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCTDGYEWDPVRQQCKDIDECDIVPDACKGGMKCVNHYGGYLCLPKTAQIIVNNEQPQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASX_HYDROXYL; 'EGF_1; FALSE_NIEGF_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (n) Calcium-binding; Glycoprotein; Siceptivial.

EGF-CONTAINING FIBULIN-LIKE EX MATRIX PROTEIN 1.

EGF-LIKE 1, DIVERGENT.

EGF-LIKE 2, CALCIUM-BINDING (PC EGF-LIKE 3, CALCIUM-BINDING (PC EGF-LIKE 4, CALCIUM-BINDING (PC EGF-LIKE 5, CALCIUM-BINDING (PC EGF-LIKE 6, CALCIUM-BINDING (PC EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22DAFD70BACF1CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1108.5;
No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GPYPAAAPPLSAPNYPT
                                  493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2e-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                       385
                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
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InterPro; IPRO00152; A InterPro; IPRO00561; E InterPro; IPRO01881; E Pfam; PF000008; EGF; 3; SMART; SM00179; EGF_11 PROSITE; PS000010; ASX_
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vandenburgh K., Cousin P., Nishimura D
Mackey D.A., Hagerman G.S., Bird A.C.,
Schorderet D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giltay R., Timpl R., Kostka G.;
"Sequence, recombinant expression and tissue
extracellular matrix proteins, fibulin-3 and
Matrix Biol. 18:469-480(1999).
                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein 1 pr
(Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular S1-5).
                                                                                                                        Genew;
                                                                                                                                  EMBL; U03877;
HSSP; P35555;
                                                                                                                                                                                      entities requires
                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                               "A single EFEMP1 mutation associated with both malattia and Doyne honeycomb retinal dystrophy."; Nat. Genet. 22:199-202(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=97001163; PubMed=8812496;

Ikegawa S., Toda T., Okui K., Nakamura Y.

"Structure and chromosomal assignment of that is highly homologous to fibrillin.";

Genomics 35:590-592(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An overexpressed gene transcript in senescent and quiescent fibroblasts encoding a novel protein in the epidermal growth like repeat family stimulates DNA synthesis."; mol. Cell. Biol. 15:120-128(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95097983; Pubme
Lecka-Czernik B., Lumpk
"An overexpressed gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFEMP1 OR FBLN3 OR FE Homo sapiens (Human).
                                                                                           MIM; 126600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT DHRD/MLVT TRP-345, AND VARIANT MEDLINE-99295941; PubMed-10369267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20068041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4 be produced by alternative splitcing.

DISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB REDISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB REDISEASE: DHAD) ALSO KNOWN AS MALATFIA LEVENTINESE (MLVT OF AN AUTOSOMAL DOWNIANT DISEASE CHARACTETA LEVENTINESE CHILDY—WHITE DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
                                                                                                                                                                                                                          ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 6
                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                     HGNC:3218;
                                                                                                                                                                        s requires a license agreement ( an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                           EPITHELIUM
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                                                                                                                                               AAA65590.1;
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              EGF_CA; 4.
EGF_like; 2
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                                                                                                                      EFEMP1
    ASX_HYDROXYL;
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Primates;
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                                                                   Asx_hydroxyl.
EGF-like.
                                                      EGF_Ca
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 D., Swiderski R.F
., Sheffield V.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a Y.;
                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                         There are no rest
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i; Hominidae;
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Silvestri
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Matches 220
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SMART; SM00179; EGF_CA; 4.
SMART; SM00001; EGF_Like; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4.
PROSITE; PS00102; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF104223; AAD45219.1; -. HSSP; P00736; 1APQ.
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Oncogene 18:3608-3616(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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NCBI_TaxID=10090;
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SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
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                                                                                                  Similarity
                          QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
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IPR000561; EGF-like.
IPR001881; EGF_Ca.
IPR001491; Thrmbomoduln.
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                                                                                                       52.9%;
52.0%;
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Calcium-binding; Glycoprotein;
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POTENTIAL.

EGGF-CONTAINING FIBULIN-LIKE EI

MATRIX PROTEIN 2:

EGGF-LIKE 1, DIVERGENT.

EGGF-LIKE 2, CALCIUM-BINDING ()

EGGF-LIKE 3, CALCIUM-BINDING ()

EGGF-LIKE 4, CALCIUM-BINDING ()

EGGF-LIKE 5, CALCIUM-BINDING ()
                                                                                                                                                                         EGF-LIKE 6, CALCIUM
BY SIMILARITY
BY SIMILAR
                                                                          Score 1272.5; DB 1;
Pred. No. 3.2e-90;
5; Mismatches 121;
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Pfam; PF00008; I
SMART; SM00179;
SMART; SM00001;
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modified and this statement is not removed;
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lung;
                                                                 InterPro;
                                                                                                                                EMBL; D89730;
HSSP; P35555;
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                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Interaction of DA41, a DAN-binding factor-like protein, S(1-5).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97415782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                        InterPro;
                                                                                                               InterPro;
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                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content in the content in
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1EMN.
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EGF-like.
EGF_Ca.
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EGF\_CA; 4. EGF\_like; 2

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InterPro; IPR000152; Asx_hydroxy1.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001491; Thrmbomoduln.
Pfam; PF00008; EGF; 4.
PRINTS; PR00907; THRMBOMODULN.
SMARR; SM00179; EGF_CA; 4.
SMARR; SM00101; EGF_11ke; 2.
PROSITE; PS00001; EGF_11ke; 2.
PROSITE; PS000022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01186; EGF_CA; 6.
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EMBL; AF093119; AAC62108.1;
EMBL; AF109121; AAF65188.1;
EMBL; BC010456; AAH10456.1;
HSSP; P35555; 1EMN.
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the European Bioinformatics Institute. Ther
use by non-profit Institutions as long a
modified and this statement is not removed
entities requires a license agreement (See h
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MEDLINE-20068041; PubMed-10601734;
Giltay R., Timpl R., Kostka G.;
Sequence, recombinant expression and tissue
extracellular matrix proteins, fibulin-3 and
matrix Biol. 18:469-480(1999).
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Submitted (JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissue-Brain;
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EGF-containing fibulin-like extracellular matrix
(Fibulin-4) (FIBL-4) (UPH1 protein).
EFEMP2 OR FBLN4.
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POTENTIAL.

EGF-CONTAINING FIBULIN-LIKE EMATRIX PROTEIN 2.

EGF-LIKE 1, DIVERGENT.

EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 4, CALCIUM-BINDING ()

EGF-LIKE 5, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()
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N-LINKED (GLCNAC...) (I
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EWDPDSOH -> TOTAN (IN REE
AQHPNECPP -> VNTQPLPT (IN
C -> W (IN REF. 2).
RSV -> AER (IN REF. 3).
S -> R (IN REF. 3).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
EGF-containing fibulin-like extracellular matrix
(Fibulin-4) (FIBL-4) (Mutant p53 binding protein
EFEMP2 OR FBLN4 OR MBP1.

Q9WVJ9;

STANDARD;

443

A

Mus musculus

(Mouse)

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

protein 1).

N

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RESULT 4

FBL4_CRIGR STANDARD; PRT; 443 AA.

ID FBL4_CRIGR STANDARD; PRT; 443 AA.

AC 055058;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

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                               Pfam; PF00008; EGF; 4.

SMART; SM00179; EGF_CA; 4.

SMART; SM00001; EGF_L1kc; 2.

PROSITE; PS00010; ASX_HYDROXYL;

PROSITE; PS00022; EGF_1; FALSE_N

PROSITE; PS01186; EGF_2; 4.
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1998) to the EMBL/GenBank/DDE-i-SUBCELLULAR LOCATION: Secreted.
-i-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                               EMBL; AF046870;
HSSP; P00736; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cricetulus.
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IPR000561;
IPR001881;
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                                                                                                                                                           Asx_hydroxyl.
EGF-like.
                                                                                                                                            EGF_Ca.
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the EMBL/GenBank/DDBJ databases
N: Secreted.
                                   FALSE_NEG.
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                               RESULT 5
FBL4_HUMAN
ID FBL4_HUMAN
ID COP5967; 075967;
DT 16-OCT-2001 (Re)
DT 16-OCT-2001 (Re)
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                               (Rel.
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                                                                                      STANDARD;
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25
443
                                 40,
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                                 sequence
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Pred. No. 1.6e
64; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATRIX PROTEIN
EGF-LIKE 1, DIV
EGF-LIKE 2, CAL
EGF-LIKE 3, CAL
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                                                                                        PRT;
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E 2. CALCIUM-BINDING
E 3. CALCIUM-BINDING
E 4. CALCIUM-BINDING
E 5. CALCIUM-BINDING
E 6. CALCIUM-BINDING
                                                                                        443
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1.6e-90;
ches 121;
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(POTENTIAL).
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300

360 380 420 440 240

261

180

201

93 120

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RESULT 3
FBL5_MOUSE STANDARD; PRT; 448 AA.

ID FBL5_MOUSE STANDARD; PRT; 448 AA.

AC 09WVH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 6-OCT-2001 (Rel. 40, Last annotation update)
DT F1bulin-5 precursor (FIBL-5) (Developmental arteries and EGF-11ke protein) (Dance).

GN EGF-11ke protein) (Dance).

GN Mus musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
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Best Local S
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InterPro; IPR001881; EGF-La.
InterPro; IPR001881; EGF-La.
Pfam; PF00008; EGF; 4.
SMART; SM00179; EGF-Like; 2.
SMART; SM00001; EGF-Like; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4
PROSITE; PS00018; EGF-L; 4.
PROSITE; PS01186; EGF-L; 4.
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Furukawa Y., Kobuke K., Tashiro K., Lu
Matsumori A., Sasayama S., Chien K.R.,
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FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
FUNCTION: THEORIES AND THE RED MOTIF. COULD BE A VASCULAR
INTERACTION OF INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
DEVELOPMENT AND REMODELING.
SUBCELLULAR LOCATION: Secreted.
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                              PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL
                                                                                                                                                                                     QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
                                                                                                                                                                                                                                                        NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
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IPR000561;
IPR001881;
GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ
                                                                                                                                                                                                                                        NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC
                                                                                                                                                                                                                                                                                                          TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI
                                                                                                   PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC
                                                                                                                                                                     QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ
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EGF-like.
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EGF-LIKE 2, CALCIUM-BINDING ()

EGF-LIKE 3, CALCIUM-BINDING ()

EGF-LIKE 4, CALCIUM-BINDING ()

EGF-LIKE 5, CALCIUM-BINDING ()

EGF-LIKE 6, CALCIUM-BINDING ()
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BY SIMILARITY

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Pred. No. 7
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( (IN REF. 3).
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Repeat; |
SIGNAL
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Q9WVH8;
 CHAIN
DOMAIN
DOMAIN
DOMAIN
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"EVEC, a novel epidermal growth factor-like repeat-containing upregulated in embryonic and diseased adult vasculature.";
Circ. Res. 84:1166-1176(1999).
-!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULIGAND.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (FVEC).
FBLN5 OR DANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
                                                                                                                                                        Interpro: IPR000152; Asx_hydroxyl.
Interpro: IPR000561; EGF-like.
Interpro: IPR001881; EGF-Ca.
Pfam; PF00008; EGF; 4.
SMART; SM00179; EGF_CA; 4.
SMART; SM00001; EGF_like; 2.
                                                                                                                                                                                                                                            EMBL; AF112153; AAD41769.1;
EMBL; AF137350; AAD25101.1;
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Addom N.L., Matsumori A., Sasayama S., Chien K.R., Honjo T.;
"DANCE, a novel secreted RGD protein expressed in devel-
atherosclerotic, and balloon-injured arteries.";
T. Biol. Chem. 274:22476-22483(1999).
2]
EQUIENTE PROCESSED IN TABLE 1.
                                                                                                                PROSITE; PS00010;
PROSITE; PS00022;
PROSITE; PS01186;
                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=99278197; PubMed=10347091;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99357779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                 LIGAND FOR INTEGRIN RECEPTORS AND MAY PL
DEVELOPMENT AND REMODELING.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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                                                                                     EGF-like domain;
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                                                                                                                ASX_HYDROXYL; 4.
EGF_1; FALSE_NEG
EGF_2; 4.
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-Lozano P., Lindner V.,
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448
69
167
206
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Rodentia;
                                                                                     Calcium-binding;
FIBULIN-5.
EGF-LIKE 1, DIVERGENT.
EGF-LIKE 2, CALCIUM-BINDING
EGF-LIKE 3, CALCIUM-BINDING
EGF-LIKE 4, CALCIUM-BINDING
                                                                         POTENTIAL
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Sciurognathi;
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thi; Muridae; Murinae; Rat
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                                                                                     Glycoprotein;
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VASCULAR
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Run

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2003, 17:40:07; Search time 10.6843 Seconds (without alignments) 1642.086 Million cell updates/sec

protein

protein search, using sw model

GenCore version Copyright (c) 1993 - 2003

Compugen Ltd 5.1.6

Minimum DB Maximum DB

seg length: 0 seg length: 2000000000

otal number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Post-processing: Minimum Match 0%

Maximum Match 100 Listing first 45

100%

summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Scoring table: Sequence: Title: Perfect score:

BLOSUM62

Gapop 10.0 , Gapext 0

US-09-674-379A-14 2407

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[3]
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Fibulian-5 precursor (FIBL-5) (Developmental arteries and neural crest
EGF-11ke protein) (Dance) (Urine p50 protein) (UP50).
FBLN5 OR DANCE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shaul Y.;
Zemel R., Sholto O., Shall Y.;
Zemel R., Shall Y
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99357779; PubMed=10428823;
MEDLINE=99357779; PubMed=10428823;
Makamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.;
MDANCE, a novel secreted RGD protein expressed in developing,
atherosclerotic, and balloon-injured arteries.";
J. Biol. Chem. 274:22476-22483(1999).
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                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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                              AJ133490; CAB38568.1; -. AF112152; AAD41768.1; -. AF093118; AAC62107.1; -.
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NTC1_RAT
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NEL2_RAT
NEL_CHICK
NTC4_MOUSE
NTC1_BRARE
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CD93_MOUSE
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· W N F	2303		444		FBL5_RAT FBL5_MOUSE
u &	1276.5 1276.5		443	<b>-</b> -	FBL4_CKIGK
<b>1</b> 0	1272.5		443		FBL4_MOUSE
œ <b>~</b>	1093.5		493	۲ ب	FBL3_HUMAN
9	769.5		684	_	FBL1_CHICK
10	729.5		1221	_	FBL2_MOUSE
11	702		705	μ.	FBL1_MOUSE
12	701.5		1184	ـ ر	FBL2_HUMAN
14	596		712	۳	FBL1_CAEEL
15	539		1394	ب	LTBS_HUMAN
16	່າຜ	22.4	2871	<b>-</b> -	FRN1 HIMAN
3 .	522.5	21.7	2871	<b>-</b>	FBN1_BOVIN
19	518	•	1712	1	1 1
20	516.5	•	2871	۲	FBN1_PIG
2 22	509.5	21.2	2871	بر د	FBN1_MOUSE
23	508.5		2911	, س	FBN2_HUMAN
24	455		956	_	
25	431	•	956	ب	MTN2_MOUSE
26	421	•	931	ب ،	EMR1_MOUSE
27	392	•	886	ىر د	EMR1_HUMAN
2 6	372	15.0	810	_,	NELL HUMAN
30	372		816	<u></u>	NEL2_MOUSE
31	369	•	2471		NTC2_HUMAN
ω ω Ν	367		810		NEL1 RAT

P00736;

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C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: A55567
R:Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
Genomics 23, 480-485, 1994
A:Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to A; Reference number: A55567; MUID:95137597; PMID:7835900
A; Accession: A55567
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-2871 <TIL>
A; Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428
C:Superfamily: fibrillin 1; EGF homology
F;1201-1236/Domain: EGF homology <EGF>
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Best Local Similarity 29.9
Conservative
                                                                                                       1331 HNCDRHAVCTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1388
1389 CL----CKEGYTGDGFTCTDLDECSENLNLC--GNGQCLNAP 1424
                                                                                                                                                                                                              1271 ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1330
                                                                                                                                                                                                                                                                                                                        1106 ------MMMKNCMDIDECQRDPLLCRGGVCLNTEGSYRCECPPGHQLAPNISA 1152
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                                                                                                                                                                                                                                                   192 ------CVQ-------TCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSE 230
                                                                                                                                                         231 FLCQHE--CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFK 288
                                                                                                                                                                                                                                                                                                                                                                                100 CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
                                                     289 CIDPIRCEEPYL-------RISDNRCMCPAENPGCRDQP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TPYSGPYPAAAPPLSAPNYPTISR----PLICRFGYQMDES------NQ: | | | | | | | | | | | | | | | |
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Search completed: July 3, 2003, 18:22:42 Job time: 17.9977 secs

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A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Nature 352, 334-337, 1991
A;Title: Partial sequence of a candidate gene for the Marfan A;Reference number: S17064; MUID:91304568; PMID:1852207
A;Accession: S17064
                                                                                                                                                                                                                                                                                                                 fibrilln 1 precursor - human (fragment)
C;Species: Homo saplens (man)
C;Date: 02-Jun-195 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198
R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 193
A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multide
A;Reference number: A47221; MUID:94010947; PMID:7691719
A;Accession: A47221
           A; Molecule type: mRNA
A; Residues: 1030-3002 <MAS>
                                                                                                                                                                                          R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Hum. Mol. Genet. 2, 961-968, 1993
A;Title: Genomic organization of the sequence coding for A;Reference number: I54355; MUID:93372860; PMID:8364578
A;Accession: I54355
A; Cross-references:
                                                                                                                                         A; Molecule type: mRNA
A; Residues: 132-3002 < PER>
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A: Residues: 1-337, 'T', 339-1029 < COR>
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(Superfamily: unassigned EGF-related proteins; EGF homology
(Keywords: alternative splicing
(750-791/Domain: EGF homology <EGF>)
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126; Conserv
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Pred. No. 4.6e-
51; Mismatches
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No. 4.6e-28;
                                                                                                                                                                                                                                                    F.; Lynch, J.; Sykes, B.;
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                                                                                                      PID:g306746
Sakai, L.Y.
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Best Local
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        CL---
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     -CKEGYTGDGFTCTDLDECSENLNLC--GNGQCLNAP
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A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB565
A;Accession: S62111
A;Molecule type: protein
A;Residues: 1166-1176, 'X', '1178-1180, 'D', '1182-1185 <LEE27
R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.P.
J. Biol. Chem. 264, 21381-21385, 1989
A;Title: Connective tissue microfibrils. Isolation and captible: Connective tissue microfibrils.
A;Reference number: A34198; MUID:90078246; PMID:2512293
A;Accession: A34198
A;Molecule type: protein
A;Residues: 565-575;1890-1892, 'I',1894-1900 <MAD>
C;Comment: Fibrillin is a major component of elastin-ass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: fibrillin 1; EGF homology
C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein
E;1-3002/Product: fibrillin (5'.region exon A splice form) (fragment) #status predict
E;132-3002/Product: fibrillin (5'.region exon C splice form) #status predicted <MATC>
E;132-307/Domain: EGF homology <EGFP>
E;1457-1492/Domain: EGF homology <EGFP>
E;2262-2295/Domain: EGF homology <EGFP>
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A;Molecule type: DNA
A;Residues: 2217-2288,'I',2290-2325 <RES>
A;Residues: 2217-2288,'I',2290-2325 <RES>
A;Cross*references: GB.S54426; NID:9264860; PIDN:AAB25244.1; PID:9264861
A;Lee, B.; Godfrey, M.; Vitale, E.; Hor1, H.; Mattel, M.G.; Sarfarazi, M.
Rature 352, 330-334, 1991
A;Title: Linkage of Martan syndrome and a phenotypically related disorder
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17062
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A; Molecule type: mRNA
A; Residues: 'VLVTVVFIFLSYNKML', 944-1444 <LEE1>
A: Cross-references: EMBL: X62008; NID: g31398; PIDN: CAB56534.1;
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A;Title: The skipping of constitutive exons in vivo induced A;Reference number: I59574; MUID:93157831; PMID:8430317
A;Accession: I59574
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CIDPIRCEEPYL------RISDNRCMCPAENPGCRDQP
                                                                                                                                                                                                                                                                                                                                                           CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYDYDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCDSGFALDSEERNCTDIDECRISPDIC-GRGQCVNTPGDFEC--KCDEGYESGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 146
                                                                                                                                                                                                                                                                                                   CTNSEGSYECSCQPGFALMPDQRSCTDIDEC-EDNPNICDGGQCTNIPGEYRCLCYDGFM
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                                                                                                               FLC-QHE-CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFK 288
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                                                                                                                                                                                                                                        -TCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSE
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f elastin-associated
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RESULT 12
T22793
                                                                                                     submitted to the EMBL Data Library, A; Reference number: Z19616 A; Accession: T22793
                                                                                                                                                         hypothetical protein F56H11.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T22793; T24489 R;Wilkinson, J.
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A;Molecule type: DNA
A;Residues: 1-589 <BAR>
A; Experimental source: R; Lloyd, C.
                                 A;Cross-references: EMBL:Z68749; PIDN:CAA92962.1; GSPDB:GN00022; CESP:F56H11.1
                                                  A; Molecule type: DNA
A; Residues: 1-798 <WIL>
                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Description: Identification of chicken and C. elegans fibulin-1 homologs and character A;Reference number: 22337
A;Accession: T43210
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                clone F56H11
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d EGF-related
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proteins; EGF homolog
                                                                                                                                                                                             15-Oct-1999 #text_change 02-Aug-2002
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R; Kanzaki, T.; Olofsson, A.; Moren, A
Cell 61, 1051-1061, 1990
A; Title: TGF-betal binding protein: a
A; Reference number: A35626; MUID:9027
A; Accession: A35626
A; Status: preliminary; not compared w
A; Molecule type: mRNA
A; Residues: 1-1394 < KAN>
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A; Experimental source: clone TO:
C; Genetics:
A; Gene: CESP:F56H11.1
A; Map position: 4
A; Introns: 14471; 12
C; Superfamily: fibulin-1; EGF hc
                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 11-Jan-2000
C;Accession: A35626
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A35626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLC-----IP---RTNPVY 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGP---YSNPYSTPYSGPYPAAAPP--
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                                                                                                                                                                                                                                                                                  QLKTTIVGAPNVLPAIRAN-----FLLQKGEKRNSAVVTLRDSLDGPQTVKLQL
                                                                                                                                                                                                                                                                                                                QATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLYMTRPIKGPREIQLDL
                                                                                                                                                                                                                                                                                                                                                     SACGLPEE --
                                                                                                                                                                                                                                                                                                                                                                                                                        IQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHDSLNKNRCNRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKGSYLCQCPPGYK
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ce: clone T05A1
                                                                                                                                                                                                                                                                                                                                                   -CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAPNHADTEVNFEL
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; MUID:90275601;
                                    compared with conceptual translation
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                                                                                     a component
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                                                                      PMID: 2350783
                                                                                     of the large latent
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                                                                                                                     с.;
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                                                                                                                       Miyazono,
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A; Residues: 1-689 <BAR>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: Z22267
A;Accession: T42760
A;Status: preliminary; translated
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| Description: Isolation of chicken and nematode fibulin-1 homologs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibulin, splice form D precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42760
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C; Superfamily
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                                                                                                                                                                                                        SYLCOCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHD
 VNIHTKSRTGVILAFNEAIIEISVSKYPF
                               VNTVINFRGSSVIR----LRIYVSQYPF
                                                                     PESVDYNLDYVGQRHFRIVQERNIG
                                                                                                -FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMIT 399
                                                                                                                                     SLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIISPIEVSRIVTHMGV
                                                                                                                                                                       SDNR-----C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV--PADI------
                                                                                                                                                                                                                              TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI 302
                                                                                                                                                                                                                                                                              TGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKG
                                                                                                                                                                                                                                                                                                         TE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF----SEFLCQHECVNQPG 242
                                                                                                                                                                                                                                                                                                                                                 EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT
                                                                                                                                                                                                                                                                                                                                                                                                                     VNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPGY
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                                                                   IVQLVKPISGP-
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C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: alternative splicing; basement membrane; extracellular
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Best Local :
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                                                                                                                                 VKLQL 673
                                                                                                                                                                    IQLDL
                                                                                                                                                                                                      NHADTEVNFELQLKTTIVGAPNVLPAIRAN-----FLLQKGEKRNSAVVTLRDSLDGPQT 668
                                                                                                                                                                                                                                       --ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGPRE 390
                                                                                                                                                                                                                                                                          SLNKNRCNRQPSACGLPEE---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAP
                                                                                                                                                                                                                                                                                                         SDNR-----CMCPAENPGCRDQPFTILYRDMDVVSGRSVP-----
                                                                                                                                                                                                                                                                                                                                              SYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHD
                                                                                                                                                                                                                                                                                                                                                                           TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI 302
                                                                                                                                                                                                                                                                                                                                                                                                                 TGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLNE-----
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27.98;
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Pred. No. 4.4e-32;
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-----NVPGSYSCTCNPGF

----DGRSCQDVNECA 187

380 171 320

337 558 500 242 440 -SCTDGYWLLEGQCLDIDECRYGY------

260

151

Length 712; Indels 202;

Gaps

61

222

matrix

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fibulin-1D precursor - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C;Accession: T43210
        Argraves, K.M.; Roark,
        图. 平. ;
     Little,
C.D.; Argraves, W.S.
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C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02-Aug-2002
C;Accession: A55184; T08744
R:Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.
Genomics 22, 425-430, 1994
A;Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mappinal Reference number: A55184; MUID:95104855; PMID:7806230
A;Accession: A55184
                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
Molecule type: mRNA
N, Residues: 1-1184 <ZHA>
A;Cross references: GB:X82494; NID:g575232; PIDN:CAA57876.1; PID:g575233
A;Cross references: GB:X82494; NID:g575232; PIDN:CAA57876.1; PID:g575233
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
                                                                                              A; Note: DKFZp586A1519.1
C; Superfamily: fibulin-
C; Keywords: alternative
F; 1-27/Domain: signal s
                                                                                                                                                                        A; Gene: GDB:FBLN2
A; Cross-references: GDB:293037;
A; Map position: 3p25-3p24
                                                                                                                                                                                                                                     A; Experimental source: adult uterus; C; Genetics:
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A;Residues: 656-719,'QDECLMGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCVD',720-853,'T',855-11
A;Cross-references: EMBL:AL050095
                                                                                                                                                                                                                                                                                                                                 A; Reference number: 216471
A; Accession: T08744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: protein DKFZp586A1519.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibulin-2 precursor - human
                                                       ;Superfamily: fibulin-2; EGF homology
;Keywords: alternative splicing; extracellular matrix
;Reywords: alternative splicing; extracellular matrix
;1-27/Domain: signal sequence #status predicted <SIG>
;28-1184/Product: fibulin-2 protein #status predicted
;905-941/Domain: EGF homology <EGF>
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                  Query Match
Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVISLPTFREFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH
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  Score
Pred.
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5; Mismatches 154;
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701.5; DB 2; No. 7.6e-39;
                                                                                                                                                                                                                                                        DKFZp586A1519
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A;Gene: GDB:FBLN1; FBLN
A;Cross references: GB278285; OMIN:1
A;Map position: 22q13 3-22q13 3
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing
F;180-214/Domain: EGF homology <EGF1>
F;485-523/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Homo sapiens (man)
C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
C:Accession: B36346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: B36346
R;Argraves, W.S.; Tran, H.; Burgess, W.H.;
J. Cell Biol. 111, 3155-3164, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Fibulin is an extracellular matrix and plasma A; Reference number: A36346; MUID:91100426; PMID:2269669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B36346
fibulin 1 precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-601 < ARG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B36346
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Best Local :
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mes 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC
                                                            TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC
                                                                                                                     QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC
                                                                                                                                                           QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
                                     -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC
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                                                                                                                                                                                                                      25.7%;
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                                                                                                                                                                                                 Score 617.5;
Pred. No. 1.4e
46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dickerson,
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                                                                                                                                                                                                                                         DB 2;
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A; Molecule type: mRNA
A; Residues: 1-1221 <PAN>
A; Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047
A; Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047
A; Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047
B: A:Sasaki, T:; Mann, K:; Murphy, G:; Chu, M.L.; Timpl, R.
Eur. J. Biochem. 240, 427-434, 1996
A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleava
A:Reference number: $74094; MUID:96439073; PMID:8841408
A:Accession: $74095
                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Aug-2002
C;Accession: A4945; S74095
R;Pan, TC; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
J. Cell Biol. 123, 1269-1277, 1993
J. Cell Biol. 123, 1269-1277, 1993
              C; Superfamily:
                               A; Molecule type: protein A; Residues: 236-238, 'X', '
                                                                                                                                                                                                                  A;Title: Structure and expression of fibulin-2, a novel extracellular matrix protein A;Reference number: A49457; MUID:94064787; PMID:8245130 A;Accession: A49457 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
A49457
fibulin-2 precursor -
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C; Superfamily: f:
C; Keywords: alte:
F; 1-29/Domain: s:
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C; Genetics:
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Best Local S
Matches 155
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;Superfamily: fibulin-1; EGF homology
;Keywords: alternative splicing; glycoprotein
;1-29/Domain: signal sequence #status predicted <SIG>
;30-683/Product: fibulin 1 splice form C #status predicted <MAT>
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485-523/Domain:
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les 155; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSSFVAKLFIFVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS
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                fibulin-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC
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13.3-22q13.3
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,240-247;260-275;336-344,'L',346-361;405-426;566-568,'EM',569-58'
2; EGF homology
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Pred. No. 2.7
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                                                                                                   matrix
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F;1-29/Domain: signal sequence #status predicted <SIG>F;30-705/Product: fibulin, splice form D #status predicted <MAT>F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status
                                                             A;Molecule type: protein
A;Residues: 28;31-49,'X',51-53;'XX',110-117;231-240,'X',242-243;339-362,'S',364-387;4
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular m
                                                                                                                                                                       A;Cross-references: EMBL:X70854; NID:g396820; PIDN:CAA50207.1; A;Experimental source: cell-line F9 teratocarcinoma R;Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R. Eur. J. Biochem. 193, 651-659, 1990 EV. J. Biochem. 193, 651-659, 1990 E. Characterization of a novel calcium-binding 90-kDa gly A;Reference number: S13814; MUID:91065369; PMID:2249686 A;Accession: S13814
                                                                                                                                                                                                                                                                                                                                                                                       R;Pan, T.C.; Kluge, M.; Žhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L. submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse protein BM-90/fibulin A;Reference number: S36440
A;Accession: S36441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: basement-membrane protein BM-90; calcium-binding pro C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision.10-Nov-1995 #text_change 02-Aug-C;Accession: S34968; S36441; S13814
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Bur. J. Blochem. 215, 733-740, 1993
A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its A;Reference number: S34968; MUID:93358897; PMID:8354280
A;Accession: S34968
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-39, 'P', 41-705 < PAW>
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A; Residues: 1-705 < PAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEGQLC
  (covalent) #status
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Query

Match

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submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse proto:
A;Accession: S78560
A;Moloco.
                                                                                                                                                                                                                                              W.Alternate names: basement-membrane protein BM-90
C;Specles: Mus musculus (house mouse)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Aug-2002
C;Accession: S78040; S78560; S36440
R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent A, Reference number: S34968; MUID:93358897; PMID:8354280
A;Accession: S78040
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C; Date: 29-May-1998 #sequence
C; Accession: I38449
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A; Residues: 1-387 < RES>
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Pred. No. 1.5e-56;
5; Mismatches 123;
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PMID:7799918
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                                                                                   calcium-dep
                                                                                                                                                        A;Reference number: A36346; MUID
A;Accession: C36346
A;Molecule type: mRNA
A;Residues: 1-683 <ARG>
A;Cross-references: GB:X53743; N:A;Cross-references: GB:X53743; N:A;Accession: A36346
A;Molecule type: mRNA
A;Residues: 1-566 <AR2>
A;Cross-references: GB:X53741; N:A;Cross-references: GB:X53741; N:
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fibulin 1 precursor, splice form C - Indian.

N;Alternate names: fibulin C
N;Contains: fibulin 1 splice form A; fibulin 1 splice form C
C;Species: Homo sapiens (man)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
C;Accession: C36346; A36346; A32826
R;Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. 111, 3155-3164, 1990
A;Title: Fibulin is an extracellular matrix and plasma glycoprot
R;Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, Cell 58, 623-629, 1989
A;Title: Fibulin, a novel protein that interacts with the A;Reference number: A32826; MUID:89354537; PMID:2527614
A;Accession: A32826
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-39, 'P', 41-685 < CHU>
A; Cross references: EMBL:X70854
C; Genetics:
A; Introns: 568/3
C; Superfamily: fibulin-1; EGF homology
C; Keywords: alternative splicing; basement membrane; calcium binding; extra F; 1-29/Domain: signal sequence #status predicted <SIC>
F; 30-685/Product: fibulin, splice form C #status predicted <MAT>
F; 98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 AVPGDSMQLAITAGNEEGFFTTRKVSHHSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNSPGSFRCECKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS
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                                                                                                                                                                         NID: g31414;
                                                                                                                                                                                                                                                                                   NID: g31418;
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                                                                                                                                         D:g31414; PIDN:CAA37770.1; Burgess, W.H.; Ruoslahti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 744.5; DB 2
Pred. No. 6.8e-42;
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                                                                                                                                                                                                                                                                                         PIDN: CAA37772.1;
                                                                                                                                                                                                                                                                                                                                                                                                     t and plasma glycoprotein with repeated
PMID:2269669
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                                                                                                                                                                         PID: 931415
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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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Best Local Sim:
Matches 618;
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862 AAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 ACAGATTCCCACCAGTGCAACCCCACCCAGATCTGCATCAATACTGAAGGCGGGTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTGTGCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 TGCCGCTTTGGATACCAGATGGATGAAAGCAACCAATGTGTGGATGTGGATGTGGACGAGTGTGCA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel:81-92-642-5466, Fax:81-92-642-5482)
Location/Qualifiers
                                                              GAGTCTGGTGCGCACCAGTGCTCCGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTAC 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                        GAGCACAGGAACCACACGTGCAAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTC 861
                                                                                                                                                TGCCCACAGGGTTACCAGCTGCTG----GCCACACGCCTCTGCCAAGACATTGATGAGTGT
                                                                                                                                                                       TGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAATGT 801
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                                                                                                                                                                                                                                                                                                                                                                                              ATGGGGGCCCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCCTGTGTCGCTGC 780
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/protein_id="BAA92880.1"
/db_xref="Gi;73880.1"
/db_xref="Gi;738921"
/translation="MLPCTSCLPGSLLLWALLLLLLGSASPQDSEEPDSYTECTDGYE
/WDDDSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVTNUCLHGEGPPPVPP
AQHPNCPGPGYEDDQDSCVPVDECAQALHOCRPSQDCHNLPGSYQCTCPDGYKRIGP
ECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNRCDMGAPCEQRCF
MSYGTFLCRCHQGYELHRDGFSCSDLDECSYSSYLCQYRCVNEPGRESCHCPQGYQLL
MSYGTFLCRCHQGYELHRDGFSCSDLDECSYSSYLCQYRCVNEPGRESCHCPQGYQLL
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LCREQPSSIVHRYMTITSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQI
NNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF"
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/db_xref="taxon:9606"
|. .1536
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rotein 1 (MBP1) reported by Gallagher et al. (Oncogene
8; 3608-16, 1999)"
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S Kostka,G.
Direct Submission
Submitted (11-FEB-1999) Kostka G., Pr.
Nax-Planck Institut fuer Biochemie, Au
Martinsried, FRG
On Mar 21, 1990 ---
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AJ132819.2
FBLN4 gene;
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                                                                                                                                                                                              CAGGCCCTGCACGACTGTCGCCCCAGCCAGCACTACCTTGCCTGGCTCCTATCAG
                                                                                CGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCCTGGATCCTATTCTTGTACATGC
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          AACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGTGCC
                                                                                                                              TGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCGAGTGTGTGGACATAGACGAGTGC
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LCREQPSSIVHRYMTITSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDFYIRQI
NNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF"
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Pred. No. 8.5e-96;
D; Mismatches 387;
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Direct Submission
Submitted (30-JUL-1999) Shinji Tanka, Kyushu University, Faculty Submitted (30-JUL-1999) Shinji Tanka, Kyushu University, Faculty Medicine, Department of Surgery II; 3-1-1 Maidashi, Higashi-ku, Medicine, Department of Surgery II; 3-1-1 Maidashi, Higashi-ku, Fukuoka 812-8582, Japan (E-mail:shinjit@surg2.med.kyushu-u.ac.jp,
                                                                                                                                              Tanaka,S.,
                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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MBP1; mutant p53 binding
Homo sapiens cDNA to mRNJ
                                                                                                           Unpublished
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Primates;
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Otein (MBP1)
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(MBP1),
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Rowal, R.C., Richardson, J.A., Miano, J.M. and Olson, E.N.

Direct Submission

Submitted (25-MAR-1999) Departments of Molecular Biology and Oncology, Internal Medicine and Pathology, UT, Southwestern McCenter, Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235-9148

Location/Qualifiers
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EVEC mRNA, complete
AF137350
AF137350.1 GI:4583
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QTCVNTYGGSTCRCDPGYEPEEDGIHCSDMDECSTSEFLOGHECVROPGSYSCSCPPG
YVLLEDNRSCQDINECEHRNHTCTELOTCYNLOGGFKCIDPIVCEBPYLLIGDNRCMC
YVLLEDNRSCQDINECEHRNHTCTFLOTCYNLOGGFKCIDPIVCEBPYLLIGDNRCMC
PARMTGCRDOPFTILFRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREF
YMRQTGPISATLVMTRPIKGPRDIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
539 a 620 c 550 g 595 t
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a novel epidermal growth factor-like repeat containing
in upregulated in embryonic and diseased adult vasculature
Res. 84 (10), 1166-1176 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="embryonic vascular EGF EVEC"
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153. .1499
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Eutheria; Rodentia;
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Pred. No. 4.7e-289;
0; Mismatches 140;
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Vascular EGF repeat-containing protein
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Sciurognathi; Muridae; Murinae;
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Diego, 9500 Gilman Drive, La Jolla,
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Nakamura,T., Yabe,D., Tashiro,K.
Direct Submission
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PAENTGCRDQPFTILFRDMDVVSGRSVPADIFOMQATTRYPGAYYIFQIKSGNEGREF
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1 669 c 595 g 649 t 2 others
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/db_xref="G1:5305675"
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/td=ns1ation="MPGLKRILTVTILALWLPHPGNAQQQCTNGFDLDRQTGQCLDID
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ECRTIERACRGDMMCVNQNGGYLCIPRTNPVYRGPYSTSYSGPYPAAAPPVPAS
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NYPTISRPLVCRFGYQMDEGNQCVDVDGCATDSHQCNPTQICINTEGGYTCSCTDGYW
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                                                                                                                                                 ATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTC
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Query match  83.2%; Score 1056.2; DB 10; Length 2478;  Best Local Similarity 89.5%; Pred. No. 2.8e-292;  Matches 1136; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  Qy  1 CAGTGCACGAATGGCTTTGACCTGGATCGCCGTGTGTAGGACAGTGTTTAGATATTGATGAA 60;	secreted protein; expressed in crest cells, balloon injured v lesions" /codon_start=1 /product."developmental arter1 /protein."developmental arter1 /protein."id="AAD41767.1" //protein_id="AAD41767.1" //protein_id="AAD41767.1" //protein_id="AAD41767.1" /protein_id="AAD41767.1" //protein_id="AAD41767.1" /	aliforni,	SOURCE Mus musculus.  SOURCE Mus musculus.  SOURCE Mus musculus.  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  REFERENCE 1 (bases 1 to 2478)  AUTHORS Nakamura,T., Ruiz-Lozano,P., Lindner,V., Yabe,D., Taniwaki,M.,  Furukawa,Y., Kobuke,K., Tashiro,K., Lu,Z., Andon,N.L., Schaub,R.,  Matesumori,A., Sasayama,S., Chien,K.R. and Honjo,T.  DANCE, a novel secreted RGD protein expressed in developing,  atherosclerotic, and balloon-injured arteries	RESULT 11 AF112151 LOCUS DEFINITION Mus musculus developmental arteries and neural crest EGF-11ke ACCESSION AF11215.1 GI:5305670 VERSION AF11215.1 GI:5305670
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 675
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM.HGSC
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NIH-MGC Project
Contact: MGC hel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
YOOn, V.S., KOWis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
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/map="C57BL/6J"
/clone="MGC:5656 IMAGE:3482574"
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Zemel, R., Sholto, O. and Shaul, Y.
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Eukaryota;
                                 Zhang, Z.
Secreted and transmembrane
                                                Baker, K.P., Chen, J., Gurney, A.L., Pan, J.,
          Genentech,
                  Patent:
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 Location/Qualifiers
                                                                         Eutheria;
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Primates;
                                                Desnoyers, L., Goddard, A., Smith, V., Watanabe, C.K.,
                                                                                                                                  2609 bp
L WO0168848.
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                                polypeptides and
                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                Wood, W.I. and
                                acids encoding
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Sequence 2 1
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Bandman,O., Corley,N.C. and Guegler
Human extracellular matrix proteins
Patent: US 6303765-A 2 16-OCT-2001;
Location/Qualifiers
1. .2550
                                                                                                                                                                                                                                                                                                                    Unknown.
Unclassified
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                         TATTTATGCATTCCCCGGACAAACCCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTCG
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Pred. No. 0;
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/Codon_start=1
/product="Unknown (protein for MGC:22412)"
/product="Unknown (protein for MGC:22412)"
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WYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPYGICINTEGGYTCSCTDGYW
LLEGQCLDIDECRYGYQQLCANVPGSYSCTCNPGFTLNEDGRRCGDVNECATBRHPCV
OTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPG
YILLDNRSCQDINECEHRNHTCNLQQTCYLLQGFKCLDFIRGLEGNEGREF
YMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPP"
S88 a 650 c 547 g 582 t
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/db_xref="taxon:9606"
/db_xref="MGC:22412 IMAGE:4693953"
/clone="MGC:22412 IMAGE:4693953"
/tissue_type="Lung"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B"
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Sequence
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Bandman,O., Corley,N.C. and Guegler,K.J.
Human extracellular matrix proteins
Patent: US 587234-A 2 16-FEB-1999;
Location/Qualifiers
1. .2550
                                                                                                                                          Unknown.
Unclassified
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                                          Similarity
TACCCATTC
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//Gb_xref="GI:5305673"
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PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQNQATTRYPGAYYIRQIKSGNEGREF
YNRQTGPISATLYNTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYYSQYPF"
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Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 36 Row: n Column: 23 This clone was selected for full length sec

information can be http://image.llnl.

be

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Dickson,
R. M.
                     Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
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Direct Submission
Submitted (01-FEB-2002) National Institutes of
Gene Collection (MGC), Cancer Genomics Office,
Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Collection (MGC), Gene Co
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Contact: MGC help desk
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Mammalia; Eutheria;
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ECRTipeacredmmcvnqnegylcipptnyrpysnyrpysgpybaapplsab

NYPTISRPLICRFCYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYW

LLEGQCLDIDECRYCYCQLCANVPGSYSCTCNFGFTLNEDGRSCQDVNECATENPCV

QTCVNTYGSFICRCDPGYELEEDGVHCSDMDEGSFSEFLCQHECVNQPGTYFCSCPPG

YILLDDNRGCDLNECEHRNHTCNLQDTCYNLOGGFKCIDPICEEPYLRISDNRCMC

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YMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF"
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Direct Submission
Submitted (09-DEC-1998) Medicine, University of California Submitted (199-DEC-1998) Medicine, CA 92093-0613, USA Diego, 9500 Gilman Drive, La Jolla, CA 92093-0613, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura, T. Ruiz-Lozano, P., Lindner, V., Yabe, D., Taniwaki, M., Fusukasanira, T. Ruiz-Lozano, P., Lindner, V., Yabe, D., Taniwaki, M., Fusukasanira, Robursokki, Masanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasanirasa
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/note="DANCE; contains 6 cbEGF
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                                                                                                                                        Direct Submission
Submitted (05-MAR-1999) Kostka G., Dept. of Protein Chemistry,
Max-Planck Institut fuer Biochemie, Am Klopferspitz, 82152
Martinsried, GERMANY
                                                                                                                                                                               Kostka, G.
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                        Homo sapiens fibulin-5.
AJ133490
AJ133490.1 GI:4490529
FIBL-5 gene; fibulin-5
                                                                                                            Unpublished
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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EFERENCE 1 (A AUTHORS L1, H TITLE EXTR JOURNAL Pate	B4086 BCUS B4086 BCUS BEFINITION BCCESSION BA4086 BEFISION BA4086 BEFISION
Li, H. and Olsen, H.S.  EXTRACELLULAR/EPIDERMAL GROWTH FACTOR LIKE PROTEIN PATENT: WO 9846746-A 1 22-OCT-1998; HUMAN GENOME SCIENCES INC (US); LI HAODONG (US)	1720 bp com Patent W09846746. 6733224
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ALIGNMENTS

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Jearch completed: July 3, 2003, 11:59:31 Job time: 283.77 secs

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Sequence

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                         The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PTCA), or myoma, hematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood computation/thrombotic activity, receptor/ligand activity, cadohelin/ The present sequence represents the coding sequence of one protein of the continuous which can be used for modulating smooth muscle cell
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The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous transuluminal coronary angioplasty (PMCA), or myoma, hematopoletic cell-regulatory activity, cytokine activity, issue generation/reparation activity, actin/inhibitin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, cadohelin/ tumour metastasis inhibiting activity; tumor inhibition, and as nutrient. The present sequence represents the coding sequence of the invention which can be used for modulating smooth muscle cell proliferation.
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                                                                 The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or retransuluminal coronary angioplasty (PTCA), or myoma, hematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation cagulation/thombotic activity, taxis and chemotaxis activity, blood tumour metastasis inhibiting activity, taxis and chemotaxis activity, candohelin/The present sequence of the invention which can be used for modulating smooth muscle
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                                                                             polypeptides, and polynucleotides encoding them, can be used e.g. to induce DNA synthesis, to regulate vascular smooth muscle proliferation, to treat Marfan syndrome, to stimulate wound healing, to restore normal neurological function after trauma or AIDS dementia, to treat ocular disorders, to treat kidney and liver disorders, to promote hair follicular development, to stimulate growth and differentiation of epidermal and epithelial cells in vivo and in vitro, for the treatment of burns, ulcers and corneal
                                                                                                                                                                                        This claimed cDNA clone codes for a human polypeptide (see AAW31705) identified on the basis of homology as a putative extracellular protein-like/epidermal growth factor-like (EEGF) protein. It was isolated from a human foetal heart cDNA library, and can be amplified from ATCC 97285 and the product cloned into vectors for expression in bacterial, insect, mammalian or plant cells. EEGF
                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding extracellular/epidermal growth factor-like protein - useful for treatment and diagnosis of e.g. wounds, neurological disease, neoplasia, psoriasis etc
                                       incisions, and to stimulate embryogenesis and angiogenesis. Nucleic acid fragments are also used as probes or primers, diagnosis and chromosome identification.
                                                                                                                                                                                                                                                                                           Claim 4; Fig 1A-D;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-512640/47.
P-PSDB; AAW31705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vascular smooth muscle proliferation; Marfan syndrome; dementia; wound healing; alopecia; neurological disorder; ocular disorder; kidney disorder; liver disorder; embryogenesis; angiogenesis;
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26-JUL-1999
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01-SEP-1999
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DB; AAB31183.
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Gerritsen ME, Goddard A;
Mather JP, Napier MA, Par
D, Watanabe CK, Williams
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Nucleotide sequence of human polypeptide PRO210

Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183; PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO130 PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO533; PRO1318; PRO1600; PRO9940; PRO533; PRO310; PRO187; PRO337; PRO1411; PRO4356; PRO2650; PRO2630; PRO2630; PRO2630; PRO5009; sapiens Location/Qualifiers 450..1796 PRO1308;

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                                                                                                                                                TTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACATC
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Baker Dan J,

: KP, Chen J J, Smith V,

'n INC.

, Desnoyers L, Goddard A, Godowski Watanabe CK, Wood WI, Zhang Z;

PJ,

Gurney

ΑL;

2001-602746/68. DB; AAU29227.

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GENENTECH

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals

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02-MAR-2000;
03-MAR-2000;
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17-SEP-1997;
18-SEP-1997;
28-OCT-1997;
12-NOV-1997;
21-NOV-1997;
                                                                                                                                                                                                                             Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; aclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditls; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217; EGF-like; ss.
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                                                                                                  17-SEP-1998;
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Similarity

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Cc arrier or excipient), a novel pro245 polypeptide (I), its agonist or carrier or excipient), a novel pro245 polypeptide (I), its agonist or cc antagonist, or their fragments, for modulating: (i) infiltration of contining the composition increases or decreases any of the effects (i): (ii). The products of the invention have anti-inflammatory (iii) T cell proliferation. The composition increases or decreases any of the effects (i): (ii): The products of the invention have anti-inflammatory of the effects (i): (iii). The products of the invention have anti-inflammatory of the effects (i): (ii): The products of the invention have anti-inflammatory of the effects (i): (iii): The products of the invention have anti-inflammatory effects (i): (ii): and its (antyagonists can distance in the products of the invention have anti-inflammatory effects (iii): (ii): (iii): (iii)
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04-JUN-1998;
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  Sequence 2509 BP;
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                                                                                                                                                                                                                                                                                                                                                    Claim 3;
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CCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGC
                                                                                                                                                                                                                                                                                          Similarity
                    Fig 1A-G;
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New polynucleotide encoding extracellular matrix protein, Enuseful in the diagnosis, prevention and treatment of immune disorders and cancer
                                                                                                                  1999-095674/08
DB; AAW94281.
                                                   ECMP-1
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This DNA encodes a human extracellular matrix protein (ECMP)-1. He cells containing a vector comprising the ECMP-1 nucleic acid are for the recombinant production of the protein. ECMP-1 and its (ant)agonists, are useful in the diagnosis, prevention, and treat of cancer and immune disorders. 79pp; English.

2550 BP; 623 A; 690 C; 596 G; 641 Η; 0 other;

100.0%;

Score 1269; Pred. No. 0;

DB

20;

Length

treatment

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GGCTCTTTCATCTGCCGCTGTGACCCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGC
                                  CAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTAC
                                                                   AATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAG
                                                                                                               TGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCCT
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polynucleotide sequence was obtained from a human secreted protein AK647 polynucleotide sequence was obtained from a human foetal kidney cDN library. AK647 homologues in chicks and rodents are involved in acr tissue development. The spatial and temporal distribution of AK647 indicated that it acts as an a modulator of smooth muscle cells in vasculogenesis during embryonic development. The primary structure AK647 consists of multiple EGF domains. The AK647 protein can be us
                                                                                                                                              Proteins, and their encoding polynucleotides, used smooth muscle cell growth, vasculogenesis, restenos
                                                                                                                                                                                                                                                                                         19-MAY-1998;
21-MAY-1998;
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                                                                                                                                        atherosclerosis
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Agostino M,
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| TACCCATTC 1529
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Merberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a nutritional source or supplement. The protein shows both inhibitory and inducing, cytokine, cell proliferation and cell differentiation activity.
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                                                                              The sequence is that encoding a secreted protein from a human fetal kidney clone AK647. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
                                             Sequence
                                                                                                                                                                                                                                                                                               Disclosure;
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Matches 1269;
                                                                                                                                               This sequence encodes the human A55 protein of the invention. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PPCA), or myoma, haematopoletic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, actin/inhibin activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, blood coagulation/thrombotic activity, tumour inhibition, and as a nutrient.

Note: The open reading frame of this sequence, as well as the mature protein coding sequence are specifically claimed in claim 4.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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11-JAN-2000;
02-MAY-2000;
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                                                                               Query Match
Best Local Similarity
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Query Match
Best Local Similarity
Matches 1269; Conserv
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                                                                                                                                                                                                                                                                                                                                      Human EEGF genomic DNA.
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                                            /*tag= c
/product= "EEGF"
/note= "Extracellular/epidermal
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n EST sequ	AAX37683	20	354	25.7	32
encoding	AAA14616	21	1358		•
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n S1-5 E	AAZ39800	21	2018	•	
cancer as	AAF18229	21	1994	•	٠
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CDNA Se	AAS21402	22	1875	•	
PRO22	AAC58583	21	1874	•	٠
cDNA sec	AAH13771	22	1707	•	371.2
a	AAX60351	20	1531	•	•
2	AAT88974	18	1525	•	371.2
encod	AAA14608	21	1480	•	371.2
EST seque	AAX37686	20	377		374.4
Human secreted exp	AAA44245	21	680	•	576.8
full-1	112	22	1538		721.4
CDNA	AAK93169	22	853	٠	
CDNA	ø	22	853	•	721.4
Human PRO protein	AAX37673	20	778		776.4
CDNA i	ABL34757	24	1260	•	•
	AAC99605	22	1254	٠	
_	AAZ61672	21	1254	٠	
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muscle	യ	21	2233	٠	٥.
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Smooth muscle pro	3938	21	1269		
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Nucleotide sequenc	Ó	22	2609		1267.4
Human DNA encodin	$\vdash$	22	2609		1267.4

## ALIGNMENTS

ABL52528 standard; cDNA; 1347

19-JUL-2002 (first entry)

Human UP50 cDNA sequence SEQ Ü NO:1.

Human; UP50; artificial vascular graft; cellular adherence factor; cell proliferating growth factor; DANCE; epidermal growth factor; EGF; developmental arteries and neural crest EGF-like protein; gene; ss.

Homo sapiens.

WO200207646-A2

31-JAN-2002

20-JUL-2001; 2001WO-IL00670

20-JUL-2000; 2000US-0620227

(MGVS-) MGVS LTD.

Flugelman MΥ, Preis ĭ Gluzman Ζ, Koren ₽, Weisz Ą Cohen

Ţ;

WPI; 2002-361632/39

Artificial vascular graft synthetic tubular element for therapy of vascular diseases, has having a surface coated with endothelial,

Search completed: July 3, 2003, 17:53:39 Job time: 207.749 secs

OY 181 ACCCCTACTCAGGTCCGTACCCAGCAGCAGCAGCACCACTCTCAGCTCCAAACTATCCC 240	Qy 121 TATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGAACCCCTACTCG 180	Qy 61 TGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTTAACCAAAATGGCGGG 120	QY 1 CAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGTGTTTAGATATTGATGAA 60	Query Match 99.9%; Score 1267.4; DB 9; Length 2609; Best Local Similarity 99.9%; Pred. No. 0; Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	; LENGTH: 2609 ; TYPE: DNA ; ORGANISM: Homo Sapien US-10-180-552-407	တ	TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERRENCE: P3430R1C153 ; CURRENT APPLICATION NUMBER: US/10/180,552	; APPLICANT: Smith, Victoria ; APPLICANT: Watanabe, Colin K. ; APPLICANT: Wood, William I. ; APPLICANT: Zhang, Zemin	; APPLICANT: Goddard, Andrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Gurney, Austin L. ; APPLICANT: Pan, James	; GENEKAL INFORMATION: ; APPLICANT: Baker, Kevin P. ; APPLICANT: Chen, Jian ; APPLICANT: Desnoyers, Luc	RESULT 15 US-10-180-552-407 Sequence 407, Application US/10180552 Publication No. US20030022300A1	1785	Db 1725 AACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCAG 1784  Oy 1261 TACCCATTC 1269			Db 1545 TTCCAAATGCAAGCCACGACCCGTACCTGGGGCCTATTACATTTTCCAGATCAAATCT 1604  OY 1081 GGGAATGAGGGCAGAGAATTTTACATGCGGCAAAAGGGGCCCCATCAGTGCCACCCTGGTG 1140		Qy 961 TTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACATC 1020
Оy	Qу Db	Qy Db	Db Oy	Оy	Qy Db	Qy Db	ОУ	Qу Дъ	Qy Db	Qy Db	Qy Db	Qy Db	Фр	Qy Db	Qy	Qy da	, Db	VQ VQ
1261 TACCCATTC 1269          1785 TACCCATTC 1793	1201 AACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCAG 1260		1081 GGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTG 1140	. 1021 TICCAAATGCAAGCCACGACCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCT 1080 	961 TTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCGCTGACATC 1020 	901 AGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCC 960 	841 TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTG 900 	781 TGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC 840 	721 CCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGC 780 	661 AGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAG 720 	601 GCCTCTTTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGC 660 	541 CAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCAACACCTAC 600 	481 GGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGC 540 	421 TGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCCT 480 	361 AATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAG 420 	301 GTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCAGATCCTGCATC 360 		241 ACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATG

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Sequence 407, Application US/10176913

Sequence 407, Application US/10176913

Publication No. US20030022298a1

GENERAL INFORMATION:

APPLICANT Baker, Kevin P.

APPLICANT Chen, Jian

APPLICANT Chen, Jian

APPLICANT Goddard, Audrey

APPLICANT Goddard, Audrey

APPLICANT Goddard, Austin L.

APPLICANT Goddard, Victoria

APPLICANT Watanabe, Colin K.

APPLICANT Watanabe, Colin K.

APPLICANT Wood, William I.

APPLICANT WOOD, William I.

APPLICANT WOOD, William I.

APPLICANT STANG, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLITIVE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C66

CURRENT APPLICATION NUMBER: US/10/176,913

CURRENT TILING DATE: 2002-06-20

PRIOR SEQ ID NOS: 612
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          AGGATCAGTGATAACCGCTGTGTGTGTCCTGCTGAGAACCCCTGGCTGCAGAGACCAGCCC
                                           TGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC
                                                                                                              CAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCCTGCGTCAACACCTAC
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APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCL

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430RLC86

CURRENT APPLICATION NUMBER: US/10/176,757

CURRENT APPLICATION NUMBER: US/10/176,757

CURRENT FILING DATE: 2002-66-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 407

LENGTH: 2609

TYPE: DNA

ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 407, Application
Publication No. US2003002
GENERAL INFORMATION:
APPLICANT: Baker, Kevin p
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Lu
APPLICANT: Goddard, Audr
APPLICANT: Godwski, Pau,
APPLICANT: Gurney, Austri
APPLICANT: Gurney, Austri
APPLICANT: Swith, Victor:
APPLICANT: Smith, Victor:
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Godowski, Paul J
Gurney, Austin I
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Query Match
Best Local Similarity
Matches 1268; Conserv Conservative 0; Mismatches Indels 0; 60

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APPLICANT: Chen, Jián
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gorney, Austin I
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
                                                                                                                                                                                                                                                                                               Prior Application removed - NUMBER OF SEQ ID NOS: 612 SEQ ID NO 407
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Best Local
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                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
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Similarity 99.9%;
                       ACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAAACTATCCC
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Godowski, Paul J
Gurney, Austin L
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SEO ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Saplen
US-10-175-738-407
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Publication No. US2003002223
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
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Best Local S
Matches 1268
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I
APPLICANT: Wood, William I
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
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Godowski, Paul J.
Gurney, Austin L.
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   APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93450R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
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Gurney, Austin L.
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APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Nustin L
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Zhang, Zemin
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TYPE: DNA
ORGANIZSM: Homo Sapien
US-10-173-706-407
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7
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Godowski, Paul J.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
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NUMBER OF SEQ ID NOS: 612
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APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
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CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wra
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-758-407
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Publication No. US20030008353A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Suriney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
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Best Local Similarity 99.9%;
Matches 1268; Conservative
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                                          TGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC 840
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 407
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
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Matches 1268;
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Lu
APPLICANT: Goddard, Audr
APPLICANT: Goddowski, Pau
APPLICANT: Godowski, Pau
APPLICANT: Gurney, Austi
APPLICANT: Pan, James
APPLICANT: Smith, Victor
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ACCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCCAAACTATCCC
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Pan, James
Smith, Victoria
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Godowski, Paul
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                             OR FILING DATE: 1999-03-08
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: 1999-06-02
OR APPLICATION NUMBER: PCT/US99/20111
OR FILING DATE: 1999-09-01
OR APPLICATION NUMBER: PCT/US99/20594
OR FILING DATE: 1999-09-08
OR FILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                             R APPLICATION NUMBER: PCT/I FR FILING DATE: 1998-12-01 FR FILING DATE: 1998-11-25 FR FILING DATE: 1998-11-25 FR APPLICATION NUMBER: PCT/I FR APPLICATION NUMBER: PCT/I FR APPLICATION NUMBER: PCT/I FR APPLICATION TO THE PCT/I FR
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R APPLICATION NUMBER: PCT/C
RR FILING DATE: 1998-09-16
RR APPLICATION NUMBER: PCT/C
RR FILING DATE: 1998-09-17
RR APPLICATION NUMBER: PCT/C
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APPLICATION NUMBER: 09/665350
THING DATE: 2000-09-18
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APPLICATION NUMBER: 09/808689
FILING DATE: 2001-03-14
APPLICATION NUMBER: 09/866028
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FILING DATE: 1998-07-14
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FILING DATE: 2001-06-19
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PRIOR

FILING DATE:

APPLICATION NUMBER: 08/933821 FILING DATE: 1997 -09-19

LING DATE: 1997-08-26

APPLICATION NUMBER: 60/169495 FILING DATE: 1999-12-07 APPLICATION NUMBER: 08/918874

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NUMBER: 09/202088 NUMBER: 09/180997: 1998-09-10

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FILING DATE: 1998-08 APPLICATION NUMBER:

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FILING DATE: 1998-09-21

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FILING DATE: 1998-07-14
APPLICATION NUMBER: 09/136801
FILING DATE: 1998-08-19
APPLICATION NUMBER: 09/136804
FILING DATE: 1998-08-19

APPLICATION NUMBER: 08/960507 FILING DATE: 1997-10-29 APPLICATION NUMBER: 09/114844

JR APPLICATION NUMBER: 60/139695
JR FILING DATE: 1999-06-15
JR APPLICATION NUMBER: 60/145070
JR FILING DATE: 1999-07-20
JR APPLICATION NUMBER: 60/145698
JR FILING DATE: 1999-07-26
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JR FILING DATE: 1999-08-17

APPLICATION NUMBER: 60/125778 FILING DATE: 1999-03-23

LING DATE:

1998-11-20

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R APPLICATION NUMBER: 60/101922
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/106032
R FPILING DATE: 1998-10-28
R APPLICATION NUMBER: 60/109304

APPLICATION NUMBER: FILING DATE: 1998-0

1998-09-10

60/099812

OR APPLICATION NUMBER: 60/081049
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/095998
OR APPLICATION NUMBER: 60/097000
OR FILING DATE: 1998-08-10
OR APPLICATION NUMBER: 60/097000
OR FILING DATE: 1998-09-09
OR APPLICATION NUMBER: 60/099601
OR FILING DATE: 1998-09-09
OR APPLICATION NUMBER: 60/099803
OR APPLICATION NUMBER: 60/099803
OR APPLICATION NUMBER: 60/099811

APPLICATION NUMBER: 60/ FILING DATE: 1998-02-09

FILING DATE: APPLICATION NUMBER:

1998-03-

60/079294 60/074092

APPLICATION NUMBER: 60/074086 FILING DATE: 1998-02-09

FILING DATE: 1997-12-16

APPLICATION NUMBER: 60/066840 FILING DATE: 1997-11-25 APPLICATION NUMBER: 60/069694

APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21

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                   CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT APPLICATION NUMBER: 10/002,796
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/05915
PRIOR FILLING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILLING DATE: 1997-09-17
PRIOR FILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/05285
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
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US-10-066-500-14
Sequence 14, Application U
Patent No. US20020177165A1
GENERAL INFORMATION:
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APPLICANT: P.Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C7
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Hanspeter Gerber
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Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
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Timothy A. Stewart
Daniel Tumas
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Nicholas F. Paoni
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Audrey Goddard
Paul J. Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David A. Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kevin
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                                                              AGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCC
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                                    SEQUENCE DESCRIPTION: SEQ ID NO: US-09-836-561-2
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US-09-836-561-2
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            Query Match
 Best Local Similarity
                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pai
                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/212,:
FILING DATE: CUDATION:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1021
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                     IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER
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OPERATING
                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                              CLONE: 45517
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/836,561 FILING DATE: 16-Apr-2001
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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APPLICANT: Bandman, Olga
Corley, Neil C.
Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
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Best Local Similarity 100.
Matches 1269; Conservative
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                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTION ENTA:
APPLICATION NUMBER: US/09/083,002
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
FELECOMMUNICATION NUMBER: P-41,323
TELECOMMUNICATION 1000 BER: P-41,323
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US-09-083-002-1
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Patent No. US20010016650A1
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APPLICANT:
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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STREET: 87 Cambri
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
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NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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VENTION: SECRETED PROTEINS
FOHENCES: 2
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Evans, Cheryl
Agostino, Michael
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Racie, Lisa A.
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Patent No. US20020165151A1
GENERAL INFORMATION:
                                                          INFORMATION FOR SEQ
                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTING Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/041,016
FILLING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/09/083,002
FILING DATE: 21-MAR-1998
                            SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pa
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                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
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                                                                      TELEPHONE: (617) 8
                                                                                                                    NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: P-41,323
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
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                  TYPE: nucleic
                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 02140
   STRANDEDNESS:
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Merberg, David
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Racie, Lisa A.
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                              pairs
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GenCore version Copyright (c) 1993 - 2003

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Result
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Maximum Match 1008
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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US-10-176-758-407
US-10-175-737-407
US-10-175-738-407
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Sequence 1, Appli
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Sequence 407, App
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TOPOLOGY: linear	o -	RISTICS:	-	; TELEPHONE: (301) 309-8509	ATION INFORMATIC	REFERENCE/DOCKET NUMBER: PF224	: ATTORNEY/AGENT INFORMATION:	; APPLICATION NUMBER: 08/839,525	; PRIOR APPLICATION DATA:	; CLASSIFICATION:	; APPLICATION NUMBER: US/09/275,805	LICATION DATA:	PatentI	SYSTEM:	₽	; COMPUTER READABLE FORM:	8	κ.		410 KEY WEST AVENUE	ADDRESSEE: HIMAN GENOME SCIENCES INC	ŭ	SECTENCES: 11	OF TAVENTION:	NVENTION: EYTRACETITITAD	LI. HAODONG	APPLICANT: OLSEN HENRIK S	z	, sequence i, appilcation us/092/3803 ; Patent No. US20010051358A1	· CONTROL COLUMN	TS-09-275-805-1	RESULT 1

99.9 2609 9 US-10-174-582-407 Sequence 407, App 99.9 2609 9 US-10-175-739-407 Sequence 407, App 99.9 2609 9 US-10-175-739-407 Sequence 407, App 99.9 2609 9 US-10-175-744-407 Sequence 407, App 99.9 2609 9 US-10-176-488-407 Sequence 407, App 99.9 2609 9 US-10-176-747-407 Sequence 407, App 99.9 2609 9 US-10-176-787-407 Sequence 407, App 99.9 2609 9 US-10-176-787-407 Sequence 407, App 99.9 2609 9 US-10-176-985-407 Sequence 407, App 99.9 2609 9 US-10-176-987-407 Sequence 407, App 99.9 2609 9 US-10-176-991-407 Sequence 407, App 99.9 2609 9 US-10-176-993-407 Sequence 407, App 99.9 2609 9 US-10-176-993-407 Sequence 407, App 99.9 2609 9 US-10-176-93-407 Sequence 407, App 99.9 2609 9 US-10-166-273-14 Sequence 407, App 99.9 2609 9 US-10-066-273-14 Sequence 407, App 99.9 2609 9 US-10-173-697-407 Sequence 407, App 99.9 2609 9 US-10-174-885-407 Sequence 407, App 99.9 2609 9 US-10-175-481-407 Sequence 407, App 99.9 2609 9 US-10-176-481-407 Sequence 407, App 99.9 2609 9 US-10-176-481-407 Seq

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; NAME/KEY: CDS
; LOCATION: 1..3753
PCT-US95-02251-2
                                                                                                                                                                                                                                                                                           Query Match 4.1%; Score 51.6; DB 5; Length 3753; Best Local Similarity 49.1%; Pred. No. 6.8e-06; Matches 166; Conservative 0; Mismatches 169; Indels 3; Gaps
2512 GTGGGCGGCAGGAAGTGCAAGAAGATATAGATGAGTG 2549
                                           2452 GGTGACTGCATCAATACCAATGGTTCCTACAGATGTCTCTGTCCCCTGGGTCATCGGTTG 2511
                                                                                          2392 AGGGATCGGAGCCGCTGTGAGGACATTGATGAATGTGACTTCCCTGCGGCCTGCATCGGG 2451
                                                                                                                                          763 CTGGATGACAACCGAAGCTGCCAAGACATCAACGAATG 800
                                                           703 CATGAGTGTGTGAACCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTG 762
                                                                                                         643 GAAGATGGCGTTCATTGCAGTGAATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAA 702
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Search completed: July 3, 2003, 17:40:02 Job time : 59.5574 secs

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Best Local S
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 5502 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REBERENCE/DOCKET NUMBER: UM:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/316,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                       y Match 4.18;
Local Similarity 47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release *1 Control of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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     3181 CGAGATGTGGACGAGTGTGCCAGCCGAGCCTCGTGCCCCACGGGCCTCTGCCTCAACACG
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                                                                                                                                                                     481 GGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCCTCAATGAGGATGGAAGGTCTTGC
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                                                        541 CAAGATGTGAACGAGTGTGCCACCGAGAACCCTG---CGTGCAAACCTGCGTCAACACC 597
                                                                                                                                                                                                                                223;
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/desc = "DNA"
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                                                                                                                                                                                                                             0; Mismatches 241;
                                                                                                                                                                                                                                                       Score 52.4; DB 5;
Pred. No. 4.8e-06;
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PCT-US95-02251-2
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                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US
FILING DATE: 30 SEP-19
CLASSIFICATION:
APPLICATION NUMBER: US
FILING DATE: 18 FEB-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
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APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UM TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release *1 ^
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                                                  STRANDEDNESS: single
                                                                                                                                                                                               TELEFAX: (713) 789-2679
TELEX: 79-0924
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                             TOPOLOGY:
                                                                                                          LENGTH:
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                                                                               nucleic acid
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     TYPE:
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RESULT 13
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                                                                                                                Sequence 1, Application US/08479722B Patent No. 6074840 GENERAL INFORMATION:
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Best Local
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APPLICANT: Y11,
APPLICANT: Y11,
TITLE OF INVENTION: LA
TITLE OF SEQUENCES:
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NAME/KEY:
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LENGTH: 3759 base pairs
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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STRANDEDNESS: single
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REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US PCT/US95/02251 FILING DATE: 21-FEB-1995
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                      763
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                                                                                                                                                                                                                                                                                                                                                                                                                                    643 GAAGATGGCGTTCATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAA 702
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hl Similarity 49.4%;
167; Conservative
                                                                                                                                                                                                                                                                                    CTGGATGACAACCGAAGCTGCCAAGACATCAACGAATG 800
                                                                                                                                                                                                                                                                                                                       GGTGACTGCATCAATACCAATGGTTCCTACAGATGTCTCTGTCCCCTGGGTCATCGGTTG
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                                                                             Yin, Wushan
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                                                                                            Bonadio, Jeffrey
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EM: PC-DOS/MS-DOS
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                   LATENT TGF( BINDING GENES, COMPOSITIONS 13
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                                                        PROTEIN (LTBP)
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                                      AND METHODS
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; LOCATION:
US-08-479-722B-1
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Best Local Similarity
Matches 223; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (713) 934-7011
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 07-JUI
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER:
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                                                                         CGAAGCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAG
                                                                                                                                     AACCAGCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAAC
                                                                                                                                                                                       GCCTGTGAAGACTTGGATGAATGTGCCCTTCCCTGGAGTCTGCCCCACAGGCGTCTGCACC
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                                                                                                                AATACTGTAGGCTCCTTCTCCTGCAAGGACTGTGACCAGGGCTACCGGCCCAACCCCCTG
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t, Suite 250
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Pred. No. 4.8e-06;
0; Mismatches 241
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241;

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Length 5499; Indels

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RESULT 11
US-08-282-141-1
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NAME/KEY: misc_feature
LOCATION: (1)...(220)
OTHER INFORMATION: n = A,T,C
US-09-404-879A-340
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US-09-404-879A-340/c
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SEQ ID NO 340
LENGTH: 220
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Best Local Similarity
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APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                  APPLICANT: Varnum, Brian
APPLICANT: Avanzi, Glancarlo
APPLICANT: Brancolini, Claudio
APPLICANT: Manifoletti, Guidalberto
TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
      NUMBER OF
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      SEQUENCES:
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                                                                                                                        Schneider, Claudio
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Pred. No. 1.4e-15;
0; Mismatches 85;
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US-08-479-722B-3
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                                                                                                                                                                                                                                       Sequence 3, Application US/08479722B Fatent No. 6074840
GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Yin, Wushan
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COUNTRY: USA
ZIP: 77040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP) TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 54.5%;
nes 164; Conservative
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                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 91320-1789
                                                                                                      CITY:
                                                                                                                      ADDRESSEE: Williams, Morgan & Amerson STREET: 7676 Hillmont, Suite 250
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                                                                               Houston : Texas
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Pred. No. 4.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE:
                                                                                                                  Query Match
Best Local Similarity
Matches 211; Conserv
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                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3373 base pair
                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kaser, Mathew
TITLE OF INVENTION: HUMAN MATRILIN-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                    LIBRARY: UTRS
CLONE: 681719
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980 ACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGCTACTGTGCCTCAGAAAACC
                          512 TTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACC
                                                                      452 ACTGCCAGCAGCTCTGTGCGAATGTTCCTGGATCCTATTCTTGTACATGCAACCCTGGTT 511
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                                                       ACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTGGCT 979
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                                                                                                                  Conservative
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                                                                                                                              8.4%;
57.7%;
                                                                                                              Score 106.8; DB 2;
Pred. No. 3.1e-23;
0; Mismatches 152;
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; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(401)

: OTHER INFORMATION: n = A,T,C or G

US-09-643-597-278
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APPLICANT: MCNeill, PATRICIA D.
TITLE OF INVENTION: COMPOSITIONS AND METHO!
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG (
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 401
TYPE: DNA
ORGANISM: Homo sapien
1008 TCCCGCTGACATCTTCCAAATGCAAGCCACGCCGACCCGCTACCCTGGGGCCCTATTACATTTT
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                                                                                                                                                                                                                                                                                                                                                                             7.0%;
Similarity 54.2%;
                                                                                                                                                                                                                                                      GGATGAAATGTGTTGGAATTATCATGGCGGCTTCCGTTGTTATCCACGAAATCCTTGTCA 92
                                                                      CCGAGAACTGCCCCAGTCAATAGTCTACAAATACATGAGCATCCGATCTGATAGGTCTGT
                                                                                                                 CAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGT 1007
                                                                                                                                                                  AGATCCCTACATTCTAACACCAGAGAACCGATGTGTTTGCCCCAGTCTCAAATGCCATGTG
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Skeiky, Yasir A.W.
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Li, Samuel X.
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Pred. No. 2.6e-18;
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LUNG CANCER
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; ORGANISM: Human
US-09-188-930-259
Sequence 1, Application Patent No. 6417342 GENERAL INFORMATION:
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SEQ ID NO 259
LENGTH: 1018
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Local Similarity 62.3%;
hes 515; Conservative
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Pred. No. 2.4e-89;
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LENGTH: 2512
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  GCCAACACCATCAATACTTTTCGGATTAAATCTGGAAAATGGAAAATGGAGAGTTCTACCTA
                                                                    GTGGTGTCAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTAC 1047
                                                                                                          CCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCAATAGTCTACAAATACATGAGC
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                                                     ATCCGATCTGATAGGTCTGTGCCATCAGACATCTTCCAGATACAGGCCACAACTATTTAT
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Query Match
Best Local Similarity
Matches 547; Conserv
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APPLICANT: SHEFFIELD, VAL C.
TITLE OF INVENTION: MACULAR DEGENERATION
FILE REFERENCE: UIA-018.02
CURRENT APPLICATION NUMBER: US/09/248,757
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 CACCAGTGCAACCCCACCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGC
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AGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTCAAATGC
                                                   GAGTTCCTCTGCCAACATGAGTGTGTGTAACCAGCCGGCACATACTTCTGCTCCTGCCCT
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                                                                                        CCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAATGTGAGCAC
                                                                                                                                                                                                       GGATATGAGCTAAGCAGTGACAGGCTCAACTGTGAAGACATTGATGAATGCAGAACCTCA
                                                                                                                                                                                                                                                                            19.0%; Score 241; DB 4; I ilarity 54.6%; Pred. No. 2.1e-65; Conservative 0; Mismatches 445;
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Best Local Similarity
Matches 617; Conserv
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APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2018 base pairs
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0436 US
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                      TGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGC
                                                                                           CAGGCCCTGCACGACTGTCGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCAG
                                                                                                                             ACAGATTCCCACCAGTGCAACCCCACCCAGATCTGCATCAATACTGAAGGCGGGTACACC
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Pred. No. 2.7e-106;
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                                                                                                                                                                                                Sequence 259, Application US/09188930A Patent No. 6150502
GENERAL INFORMATION:
                                                    APPLICANT: Watson, James D.
APPLICANT: Sleeman, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: Olsen, et
                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versior
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,963C
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/05033
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BTOOKES, A. AndES:
NAME: BTOOKES, A. BT
  TELEFAX: 301-30
INFORMATION FOR SEQ
SEQUENCE CHARACTER
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TITLE OF INVENTION: Extr
TITLE OF INVENTION: HCAB
NUMBER OF SEQUENCES: 9
                                                               REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 208
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CITY: Rockville
STATE: MD
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Best Local Similarity
Matches 617; Conserv
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TACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGG 1161
                                                                                      GTCTACCCCGGTGCCTACAATGCCTTTCAGATCCGTGCTGCAGAACTCGCAGGGGGGGACTTT
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pred. No. 2.3e-106;
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: Compositions For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF 580 ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENTH: 1260
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                                                                                                                                                                                                     TGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC
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                                                                                              AGGATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCC
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                                               TTTACCATCTTGTACCGGGACATGGACGTGGTGTCAGGACGCTCCGTTCCCGCTGACATC
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LIBRARY: CORNNOT01

COONE: 45517

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US-09-212-168-2
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                                              Matches 1269;
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL-INFORMATION:
                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/88.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7.
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 GGGAATGAGGGCAGAGAATTTTACATGCGGCAAACGGGCCCCATCAGTGCCACCCTGGTG
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                       Score 1269;
Pred. No. 0;
0; Mismatches
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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US-08-652-877-89

US-08-652-877-87

US-08-652-877-83

US-08-652-877-83
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PCT-US95-02251-17
PCT-US95-02251-2
US-08-199-780-2
US-08-316-650-2
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US-09-248-757-1

US-08-897-443-2

US-09-643-597-278

US-09-643-597-278

US-09-644-879A-340

US-08-282-141-1

US-08-479-722B-3
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US-09-212-168-2
US-09-188-930-67
US-08-833-963C-1
US-08-980-514-2
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6646.008 Million cell updates/sec
                               Sequence 2, Appli
Patent No. 5177197
Sequence 17, Appl
Sequence 87, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 87, Appl
Sequence 83, Appl
Sequence 83, Appl
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Sequence 2, Appli
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Patent No. 158/2234 Security September 158/2234 Security September 158/2234 Security September 158/234 September 158/23
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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Incyte Pharmaceuticals,

Result No.

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US-08-307-444A-6	US-08-587-389-7	US-08-307-444A-7	US-08-587-389-8	US-08-307-444A-8	US-08-312-870-6	US-08-843-417-1	5258288-2	US-09-363-316B-23	US-09-363-316B-5	US-09-249-697A-18	US-09-249-697A-5	US-09-363-316B-2	US-09-249-697A-2	US-09-634-920-3	US-09-284-819-8	US-09-381-779-1	US-08-872-757-3
6	7.	•	8	Sequence 8, Appli	Sequence 6, Appli		Patent No. 5258288		5, 2	18,	Sequence 5, Appli	2	2	ω.	œ	Sequence 1, Appli	Sequence 3, Appli

## ALIGNMENTS

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; TOPOLOGY: linea; IMMEDIATE SOURCE: CORNNO; CLUBEARY: CORNNO; CLOME: 45517
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSED FOR WINDOWS Version 2.
CURRENT APPLICATION NUMBER: US/08/884,072
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATTRIBUTE ATT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: Palo Alto
CTATE: CA
TASA
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2550 base pairs
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linear
     100.0%;
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Score 1269;
Pred. No. 0;
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